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| *** | (TM) | ***** |
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:34:45 2000; MasPar time 7.31 Seconds 505.226 Million cell updates/sec Tabular output not generated. Run on:

Title: Description: Perfect Score: Sequence:

>US-09-016-869a-2 (1-156) from USO9016869a.pep 1078 1 MDPAAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

PAM 150 Gap 11 Scoring table:

188963 segs, 23686106 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq36 1:geneseqp Database:

Mean 31.169; Variance 144.272; scale 0.216 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Pred. No. | 1.18e-85 | 1.20e-84 | 1.20e-84 | 1.20e-84 | 1.20e-84 | 1.20e-84 | 2.26e-84 | 2.26e-84 | 9.86e-84 | 9.86e-84 | 9.86e-84 | 9.86e-84 | 9.86e-84 | 9.86e-84 | 9.86e-84 | 9.86e-84 | 1.22e-83 | 4.31e-83 | 6.65e-82 | 2.90e-81 | 2.90e-81 | 2.90e-81 | 2.59e-71 |
|---------------------|-----------------------|------------------------|---------------------|------------------------|-----------------------|------------------------|------------------------|----------|------------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|-----------------------|-----------------------|-----------------------|------------------------|------------------------|-----------------------|------------------------|-----------------------|
| Description | Cell-cycle regulatory | A human multiple tumou | Human MTS1 protein. | Amino acid sequence of | Human multiple tumour | Tumour suppressor pl6. | Human p27-p16 fusion p | • | Truncated p27/p16 fusi | Truncated p27/p16 fusi | Truncated p27/p16 fusi | CDK inhibitory fusion | Human pl6p27 fusion pr | Human pl6p27 fusion pr | Human p16(GS)p27 fusto | CDK inhibitory fusion | Human multiple tumour | Human multiple tumour | Truncated p27/p16 fus1 | Multiple tumour suppre | Human multiple tumour | Inhibitor of cyclin de | Cell-cycle regulatory |
| a | R85116 | W80524 | W40524 | W74549 | W19251 | W10627 | W95094 | W23534 | W95105 | W95106 | W95103 | W23536 | W95096 | W95107 | W95095 | W23535 | W19252 | W19253 | W95104 | R81701 | R80940 | R53401 | R85114 |
| 80 | - | Н | Н | - | ч | Н | н | ч | Н | - | -1 | н | н | - | - | ч | Н | н | - | -1 | Н | ч | - |
| Length DB | 156 | 156 | 156 | 156 | 156 | 156 | 391 | 391 | 237 | 252 | 334 | 365 | 365 | 365 | 380 | 380 | 156 | 156 | 348 | 148 | 148 | 151 | 157 |
| 9 Query Match | 100.0 | 0.66 | 0.66 | 0.66 | 0.66 | 0.66 | 98.7 | 98.7 | 98.1 | 98.1 | 98.1 | 98.1 | 98.1 | 98.1 | 98.1 | 98.1 | 98.0 | 97.4 | 96.2 | 95.5 | 95.5 | 95.5 | 85.4 |
| Score | 1078 | 1067 | 1067 | 1067 | 1067 | 1067 | 1064 | 1064 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1057 | 1056 | 1050 | 1037 | 1030 | 1030 | 1030 | 921 |
| Result No. | П | 7 | m | 4 | S | ω | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 |

| 24 | 737 | 68.4 | 130 | 7 | 511 | Cell-cycle regulatory | .33e- | |
|-----------------------|-------------|-----------|----------|---|------------|------------------------|----------|--|
| 25 | 735 | | 105 | Н | W74550 | Amino acid sequence 1 | .02e- | |
| 56 | 735 | | 105 | Н | R80947 | Human multiple tumour | .02e- | |
| 27 | 735 | | 105 | Н | W19254 | Human multiple tumour | .02e- | |
| 28 | 735 | | 105 | - | W40525 | Human MTS1E1-beta prot | 'n | |
| 59 | 735 | | 105 | Н | R81700 | Multiple tumour suppre | .02e- | |
| 30 | 735 | | 105 | н | W80525 | Φ | .02e- | |
| 31 | 729 | 67.6 | 130 | ~ | W70823 | Mouse multiple tumour | | |
| 32 | 725 | 67.3 | 138 | Н | R80948 | Human multiple tumour | 1.62e-53 | |
| 33 | 725 | | 138 | Н | W80526 | A human multiple tumou | • | |
| 34 | 725 | 67.3 | 138 | н | R81702 | Multiple tumour suppre | 1.62e-53 | |
| 35 | 725 | 67.3 | 138 | н | W74553 | d sequ | . 62e | |
| 36 | 725 | 67.3 | 138 | н | W40526 | | . 62e | |
| 37 | 725 | 67.3 | 138 | Н | W19255 | | . 62e | |
| 38 | 713 | 1.99 | 138 | Н | R85117 | Cell-cycle regulatory | 1.97e-52 | |
| 39 | 9/9 | | 168 | ч | W80527 | Mouse multiple tumour | .31e-4 | |
| 40 | 556 | 51.6 | 138 | ч | R85115 | Cell-cycle regulatory | . 58e- | |
| 41 | 484 | 44.9 | 67 | Н | W16324 | Human INK4a-p16 C-term | .67 | |
| 42 | 473 | 43.9 | 125 | н | W16322 | Murine INK4a-p16 C-ter | | |
| 43 | 473 | 43.9 | 125 | Н | R85120 | Cell-cycle requiatory | .31 | |
| 44 | 446 | 41.4 | 85 | н | R85113 | | 1.54e-28 | |
| 45 | 446 | | 127 | Н | R85119 | | 1.54e-28 | |
| | | | | | | | | |
| | | | | | ALIGNMENTS | | | |
| RESULT 1 ID R85116 | 1 116 st | standard; | Protein; | | 156 AA. | | | |
| | :01 | | | | | | | |

| RESULT | |
|--------|--|
| g g | R85116; R85116; |
| 뒴 | 1996 (first e |
| 凹 | protein p16. |
| K | cycle re |
| K | cell pro |
| SO | Homo saptens. |
| PN | WO9528483-A1. |
| G. | |
| PF | |
| PR | 14-APR-1994; US-227371. |
| PR | |
| PR | |
| PR | 29-NOV-1994; US-346147. |
| PA | OLD SPRING HARBOR LAB. |
| PI | Beach DH, Demetrick DJ, Hannon GJ, Serrano M; |
| DR. | WPI; 95-373798/48. |
| ä | N-PSDB; T02962. |
| F | New cell cycle regulating proteins bind to cyclin dependent kinase - |
| P | and related nucleic acids, antibodies etc., used in diagnosis and |
| PŢ | therapy of abnormal cell proliferation, degeneration etc. |
| PS | Claim 1; Page 76-77; 109pp; English. |
| ខ្ព |) protein p16 (R85116) |
| ខ | obtd. by expression of a cDNA clone (T02962) isolated in a 2-hybrid |
| ႘ | screening assay. CCR p16 specifically inhibits the activity of |
| ខ | cyclin-dependent kinases during various stages of the cell cycle, |
| ႘ | and can be used in the treatment and diagnosis of proliferative |
| ပ္ပ | |
| S S | Sequence 156 AA; |
| õ | Ouerv Match 100.0%: Score 1078: DB 1: Length 156: |
| Wa Be | Similarity 100.0%; Pred. No. 1.18e-85; 56; Conservative 0; Mismatches 0; |
| g | 1 MDPAAGSSNEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 60 |
| ογ | 1 MDPAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 60 |
| q | 61 ELLILHGAEPNCADPATITRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120 |
| | |
| ογ | 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120 |
| q | 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156 |
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MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
familial melanoma locus; MLM; predisposition.
Homo sapiens.
14-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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This sequence represents a human multiple tumour suppression protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoms, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVWMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 65-66; 80pp; English.
The present sequence represents a human multiple tumour suppressor (WTG1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design
                                                                                                                                                                                                       01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
07-JUN-1995; US-487033.
UKTR.) MRRAD GENETICS INC.
JIANG P. Kamb A, Stone S;
WPI, 99-044585704.
N-PSDB; V70583.
Mouse multiple tumour suppressor gene segment - useful for primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1067; DB 1; Length 156
Pred. No. 1.20e-84;
1; Mismatches 1; Indels
                                                                                          A human multiple tumour suppressor 1 (MTS1) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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W40524;
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W80524 standard; Protein; 156
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Best Local Similarity 98.7%;
Matches 154; Conservative
                                                             (first entry)
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07-JUN-1995; US-487033.

18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; WS-227369.
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wpi: 98-250421/22.
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                                                                                                                                                       Homo sapiens.
US5843756-A.
                                                             03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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mutation(s)

Subscioure; Column 63-64; 73pp; English.

This is the amino acid sequence of the multiple tumour suppressor I rhis is the amino acid sequence of the multiple tumour suppressor I committed in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used to screen for drugs to be used for cancer therapy, and the protein screen for drugs to be used for cancer therapy, and the protein selection in a cell.
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                                                                                                                                                                                     ö
MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosts of predisposition to cancers. e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                                                                                                                                                                                             1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVA 60
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04-DEC-1998 (first entry)
Amino acid sequence of multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
somatic mutation; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                         1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVA
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                                                                                                                                                    Length 156;
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                                                                                                                                                Score 1067; DB 1; Length 15
Pred. No. 1.20e-84;
1; Mismatches 1; Indels
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W74549 standard; Protein; 156 AA.
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                                                                                                                                                Query Match
Best Local Similarity 98.7%;
Matches 154; Conservative
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07-UTN-1995; 480810.

07-UTN-1995; US-480810.

18-MAR-1994; US-215086.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UTN-1994; US-227369.
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156 AA;
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W09906540-A2.
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Tumour suppressor; p16; 1nhibitor; cyclin-dependent kinase 4; CDK4;

Tumour suppressor; p16; 1nhibitor; cyclin-dependent kinase 4; CDK4;

cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
anti-anglogenic activity; hyperproliferative disorder.

Homo saplens.

W09703635-A2.
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                ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE
                                   ö
                                                                                                                                                                                                                                                                                Human multiple tumour suppressor 1 gene product.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s) Claim 1; Columns 61-64; 72pp; English.
The present sequence the human multiple tumour suppressor 1 (MTS1) gene product, useful in cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1067; DB 1; Length 156;
Pred. No. 1.20e-84;
1; Mismatches 1; Indels
                                                                                                                 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                              LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD
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                                                                                                                                                                                                                   standard; Protein; 156 AA.
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18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
17-MAR-1995; WO-003537.
07-JUN-1995; US-474177.
(MYRI-) MYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
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17-JUL-1996; US-502881.
(TEXA ) UNIV TEXAS SYSTEM.
JIN X, ROLH J;
WPI: 97-132336/12.
N-PSDB; TG0951.
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Best Local Similarity
Matches 154; Conser
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N-PSDB; T72311
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Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoms.

To bladder cancer or melanoms.

This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in enkaryotic cells and used in the expression construct of the invention. p16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the capression construct inhibits p16 function. Reduced or increased levels of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
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Whaman p27-p16 fusion protein.

Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis;

Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis;

CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;

intracellular; transcellular; transcytosis; vascular wound; repair; hair;

smooth muscle; cardiovascular; arterlosclerotic; fibroriacide;

cellular proliferation; rheumatcoid arthritis; diabetes; cirrhosis; graft;

tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Librosis and neurodegeneration of city, result injust, cancers, fibrosis and neurodegeneration claim 63; Page 70-72; 88pp; English.

Claim 63; Page 70-72; 88pp; English.

Claim 63; Page 70-72; 88pp; English.

(CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1067; DB 1; Length 156;
Pred. No. 1.20e-84;
1; Mismatches 1; Indels
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29-UUL-1998; US-902572.
29-UUL-1997; US-902572.
(MITO-) MITOTIX INC.
Beach DH, Gyuris J, Lamphere L;
WPI; 99-153770/13.
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Best Local Similarity 98.7%;
Matches 154; Conservative
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cally ended to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (1) a therapeutic collypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (il) a transcellular process when FP enters the cell, and (il) a transcellular consists of at least one CDK-binding motif and a TCP. (A) are used to creat yacquiar wounds that involve a break in the endothelium and excessive proliferation of smooth muscle, particularly restenosis but more generally any repair of cardiovascular damage, arteriosclerottic correspond or for endothelialisation of synthetic vascular graffs. More generally, FP are used to treat unwanted cellular proliferation in a very wide range of situations, e.g. for treating vascular diseases as above; confront allocated arthritis, diabetes, cirrhosis); many tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration; corne; also to control hair growth (e.g. to prevent hair loss caused by chemotherapy or radiation); periodontal disease; to treat tachycardia; to inhibit spermatogenesis etc. Chimeeric proteins comprising CDK-binding motifs from two or more different proteins bind to CDKs so inhibit cell correspond to produce FP in cell cultures, for production or for regulating cell differentiation in vitro. The present cell sequence represents a human p27-p16 fusion protein.
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This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) binding motifs from at least two different proteins that bind to CDKs. The protein controls prollferation and/or differentiation of cells, 16-MAR-1998 (first entry)
CDK inhibitory fusion protein #1.
Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
chimeric polypeptide; human; binding motif; proliferation control;
cell differentiation; cell-cycle inhibitor; proliferative disorder; Chimeric inhibitor of cyclin dependent kinase - useful for gene therapy of cancer and other proliferative and differentiative diseases /note= "(Gly4Ser)2 linker" note- "poly-His tag" Claim 40; Page 38-40; 58pp; English. Location/Qualifiers 31-JUL-1997. 17-JAN-1997; 000569. 23-JAN-1996; US-58981. (MITO-) MITOTIX INC. Beach D. Gyuris J, Lamphere L; WPI: 97-393665/36. N PSDB; T74051. W23534 standard; Protein; 391 AA. W23534; tissue degeneration; therapy .219 Misc_difference 205 Misc_difference 1 Homo sapiens. WO9727297-A1.

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fibrosis and neurodegeneration.

Claim 63; Page 85; 88pp; English.

Claim 64; Particularly CDK/cyclin complexes. It provides a recombinant comprising a sequence encoding an inhibitory polypeptide containing at large comprising a sequence encoding an inhibitory and thibiting at large 11; (11) a second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (111) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (1) a therapeutic collypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (11) a transcellular process when FP enters the cell, and (11) a transcellular process when FP enters transcytosis of FP. The FP
particularly they inhibit cell-cycle progression. They can be used to treat a wide range of proliferative disorders, eq. cancer, leukaemia, psorlasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation etc. They degeneration of tissue, eq. Alzheimer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically context various forms of folliculitis, and to inhibit spermatogenesis or obgenesis. The chimeric proteins can also be used in vitro to maintain cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK/cyclin complex than binding motifs used individually (since they may bind to CDK involved in different stages of
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Truncated p27/p16 fusion protein.
Truncated p27/p16 fusion protein.

Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhibitory; restenosis; Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhracellular; candothalialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatiof arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.7%; Score 1064; DB 1; Length 391; Best Local Similarity 98.7%; Pred. No. 2.26e-84; Matches 154; Conservative 1; Mismatches 1; Indels
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W95105 standard; Protein; 237 AA.
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Beach DH, Gyuris J, Lamphere L;
WPI; 99-153770/13.
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29-JUL-1998; U15759.
29-JUL-1997; US-902572.
                                                                                                                                                                                                                                                                                                                                                                                          the cell cycle)
Sequence 391
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Fugion and chimaeric proteins including cyclin-dependent kinase
Dinding motif - used for regulation of cell proliferation and
Afferentiation, for treatment of, e.g. vascular injury, cancers,
fibrosis and neurodegeneration

Figure invention relates to novel inhibitors of cyclin-dependent kinases
Claim 63; Page 85; 88pp; English.

Claim 63; Page 85; 88pp; English.

Claim 63; Page 85; 88pp; English.

Comprision system (A) that complexes. It provides a recombinant
transfection system (A) that comprises: (1) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
comprising a sequence encoding an inhibitory polypeptide chair
CC linked to a transcription regulator functional in enkaryotic cells; (ii)
Second gene construct comprising a sequence encoding a polypeptide that
promotes endothelialisation, and (iii) a gene delivery composition for
Cd delivering the GCs to a cell for transfection. Also provided are nucleic
acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC acids encoding a fusion man intranscluluar procent that alters a
C callular process when FP enters the cell, and (ii) a transcellular
C consists of at least one CDR-binding motif and at TCP. See X26220 for
C detailed uses of the recombinant transfection system. The present
C sequence represents a human truncated p27/pl6 fusion protein.
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Truncated p27/p16 fusion protein.
Truncated p27/p16 fusion protein.
Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis; Cyclin-dependent kinase, CDK, CDK-cyclin complex; therapeutic; acne; intracellular; transcellularis; transcytosis; vascular wound; repair; hair; semoch muscle; cardiovascular; arterioscierotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; trachycardia; human; p27; p16; truncated.
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                                                                                                                                                                   Gaps
consists of at least one CDK-binding motif and a TCP. See X26220 fo detailed uses of the recombinant transfection system. The present sequence represents a human truncated p27/p16 fusion protein. Sequence 237 AA;
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                                                                                                                  Length 237;
                                                                                                                Score 1057; DB 1; Length 23
Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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29-UUL-1997; US-902572.
(MITO-) MITOTIX INC.
Beach DH, Gyuris J, Lamphere L;
WPI; 99-153770/13.
                                                                                                                Query Match
Best Local Similarity 99.4%;
Matches 154; Conservative
                                                                                                                  Query Match
Best Local Similarity
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Claim 63; Page 83; B8pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases the invention relates to novel inhibitors of cyclin-dependent kinases (CDKS), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in enkaryctic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothellalisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapettic collypeptide sequence (TP) from an intraccillular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular collypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP, see x26220 for detailed uses of the recombinant transfection system. The present
                                                                                                                                                                                                                                                          25-MAY.1999 (first entry)
Truncated p27/p16 fusion protein.
Truncated p27/p16 fusion protein.
Truncated p27/p16 fusion protein.
Truncated p27/p16 fusion protein.
CDK-binding motif: endothelialisation; fusion protein; therapentic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arterioscierotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; qraft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated.
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240 LLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEEL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 334;
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Pred. No. 9.86e-84;
0; Mismatches 1; Indels
                                                                                                            122 GHRDVARYLRAAAGGIRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 334
                                                                                        GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saptens,

W09906540-A2.

11-FEB-1999,

29-JUL-1998; U15759.

29-JUL-1997; US-902572.

(MITO-) MITOTIX INC.

Beach DH, Gyuris J, Lamphere L;

WPI; 99-153770/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrosis and neurodegeneration
                                                                                                                                                                                                                       W95103 standard; Protein; 334 W95103;
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W23536 standard; Protein; 365
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Best Local Similarity 99.4%;
Matches 154; Conservative
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                                                                                        218
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Gaps

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Score 1057; DB 1; Length 252; Pred. No. 9.86e-84;

98.18;

99.48;

Sest Local Similarity

154; Conservative

Matches

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à

98 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAE 157

0; Mismatches

2 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAE 61

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29-JUL-1998;
29-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) binding motifs from at least two different proteins that bind to CDKs. The protein controls proliferation addord differentiation of cells, carticularly they inhibit cell-cycle progression. They can be used to particularly they inhibit cell-cycle progression. They can be used to proliferative disorders, e.g. cancer, leukaemia, com also treat diseases associated with de-differentiation or can also treat diseases associated with de-differentiation or citissue, e.g. Alzheimer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and correct various forms of folliculitis, and to inhibit spermatogenesis or to treat various forms of folliculitis, and to inhibit spermatogenesis or cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK-Cyclin complex than binding motifs used the confidence of the CDK-Cyclin complex than binding motifs used the confidence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pl6p27 fusion protein.

Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; Cyclin-dependent kinase; CDK; CDK, CDK; CDK binding motif; endothebilalisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcellular; transcellular; transcellular; transcellular; transcellular; acadiovascular; actaloscelerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; tumour; inflammation, neurodegeneration; periodontal; spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                    pl6 gene;
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                     16-MAR-1998 (first entry)
CDK inhibitory fusion protein pl6p27.
CDK inhibitory fusion protein pl6p27.
Fusion gene, CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gchimeric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder; tissue degeneration; therapy.
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Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 40; Page 46-48; 58pp; English.
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WPI; 97-393685/36.
N-PSDB; T74053.
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Best Local Similarity 99.4%;
Matches 154; Conservative
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                                                                                                                                                                                                                                                                   31-JUL-1997,
17-JAN-1997, U00569.
23-JAN-1996, US-589981.
(MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric inhibitor of
therapy of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AA;
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WO9906540-A2
                                                                                                                                                                                                         sapiens
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Claim 63; Page 78-79; 88pp; English.

Claim 63; Page 78-79; 88pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases

CC (CDKS), particularly CDK/cyclin complexes. It provides a recombinant

transfection system (A) that comprises: (I) first gene construct

transfection system (A) that comprises: (I) first gene construct

comprising a sequence encoding an inhibition activity of a CDK,

comprising a sequence encoding an inhibition activity of a CDK,

comprising a sequence encoding and inhibiting activity of a CDK,

consistent comprising a sequence encoding a polypeptide that

consistent the GCs to a cell for transfection. Also provided are nucleic

delivering the GCs to a cell for transfection. Also provided are nucleic

collular process when FP enters the cell, and (ii) a transcellular

collupar process when FP enters the cell, and (ii) a transcellular

collular process when FP enters the cell, and (ii) a transcellular

consists of at least one CDK-binding motif and a TCP. See X2620 for

consists of at least encombinant transfection system. The present
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binding motif - used for regulation of cell proliferation and
differentiation, for treatment of, e.g. vascular injury, cancers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1057; DB 1; Length 365;
Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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W95107 standard; Protein; 365 AA.
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Claim 63; Page 86; 88pp; English.
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                                                                              Beach DH, Gyuris J, Lamphere L; WPI; 99-153770/13.
                                                                                                                                                                                                                                                                                                     fibrosis and neurodegeneration
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Human p16p27 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 98.1%;
1 Similarity 99.4%;
154; Conservative
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US-902572.
                                       (MITO-) MITOTIX INC.
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29-JUL-1997; US-9025
(MITO-) MITOTIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 AA;
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                                                                                                                                                    N-PSDB; X26224
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US-09-016-869A-2.rag

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comprising a recombinant complexes. It provides a recombinant transfection system (A) that comprises: (I) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothalialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular consists of at least one CDK-binding motif and a TCP. See x26220 for detailed uses of the recombinant transfection system. The present
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WESURY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to novel inhibitors of cyclin-dependent kinases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1057; DB 1; Length 365;
Pred. No. 9.86e-84;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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W95095 standard; Protein; 380 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 18: Mailarity 99.4%; March 194; Conservative
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29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; X26223
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WO9906540-A2.
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polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDF-binding motif and a TCP. See X26220 for detailed uses of the recombinant transfection system. The present sequence represents a human p16(GS)p27 fusion protein.
                                                                                                                                                            12 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAE 71
                                                                                                                                                                                         61
                                                                                                                               Gaps
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                                                                                                Length 380;
                                                                              Score 1057; DB 1; Lengtn sov
Pred. No. 9.86e-84;
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Best Local Similarity 99.4%;
Matches 154; Conservative
                                                             380 AA;
                                                               Sequence
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Search completed: Thu Jul 20 08:34:54 2000 Job time : 9 secs.

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| | protein - protein database search, using Smith-Watern Thu Jul 20 08:36:50 2000; MasPar time 5.60 Secc ut not generated. >US-09-016-869A-2 (1.165) from US09016869A.pep | 1.750) IIOM USUGULDEBDYA. 1078 1 MDPAAGSSMEPSADWLATAA PAM 150 Gap 11 145341 seqs, 14437480 res | ing: Minimum Match 0% Listing first 45 summaries a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5 Mean 29.074; Variance 136.818; scale 0.21 No. is the number of results predicted by chance greater than or equal to the score of the result | A CHAIVED DY ANALYSIS OF THE COTAL SCONDANTES Query Query CHAICH Length DB ID DESCRI 100.0 156 3 US-08-891 Sequen 100.0 156 2 US-08-892 Sequen 100.0 156 2 US-08-895 Sequen 100.0 156 2 US-08-895 Sequen 100.0 156 2 US-08-895 Sequen 100.0 156 1 US-08-480 Sequen 100.0 156 1 US-08-480 Sequen 100.0 156 1 US-08-898 Sequen 100.0 156 1 US-08-154 Sequen 100.0 1 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: P.C. FORM:
SOFTWARE: ASCII(text)
CORREMING SYSTEM:
APPLICATION DATA:
APPLICATION NUMBER: P.C. FUSS 5/04636
FILING DATE:
Sequence 14, Applicati
Sequence 47, Applicati
Sequence 47, Applicati
Sequence 64, Applicati
Sequence 16, Applicati
Sequence 6, Applicati
Sequence 6, Applicati
Sequence 4, Applicatio
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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GENERAL INFORMATION:
APPLICANT:
MOLECULE TYPE: protein
FENCE 156 AA; 16560 MW; 98948 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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GY: linear
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                         Sequence 2, Application US/08581918A
Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Benetrick, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                   156 AA
                                                121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                       PAPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                            ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                   Sequence 2, Application US/08581918A
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
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Patent No. 5962316
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 11
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIF: O2109
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                                                                                                                                                                                      Length 156;
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Pred. No. 4.93e-85;
0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: S6,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TOPPAGATION:
TELEFAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
REFERENCE/DOCKET NUMBER: MIV-071.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08305511A
         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-1290
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 anino acids
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                                                                                                                                                                                   Match 100.0%;
Local Similarity 100.0%;
Nes 156; Conservative
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Sequence 2, Application US/08627610
Patent No. 5919997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: BOS State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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Pred. No. 4.93e-85;
0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION INFORMATION:
                                                          NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPRA: (617) 832-1000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
               FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08627610
                                                                                                                                                                                                                                      156 amino acids
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Best Local Similarity 100.0%;
Matches 156; Conservative
                                                                                                                                                                                                                                                          amino acid
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ZIP: 02109
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                                                                                                                                                                                         0; Gaps
                                                                                                         Length 156;
                                                                                                                                                 Indels
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APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                    Score 1078; DB 2; L
Pred. No. 4.93e-85;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 AA
                                                                                                                                                                                                                                                                                                                                                                 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: FOLEY, HOAG & ELIOT LLP STREET: One Post Office Square CITY: Boston STATE: MA COUNTRY: USA LIFE STATE: MA COUNTRY: USA LIFE STATE: MA COUNTRY: USA LIFE STATE: MA COUNTRY: USA CONGUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LEM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION NUMBER: US/08/893,274 FILING DATE: 15-UULY-1997 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/248,812 FILING DATE: 14-SEPTEMBER-1994 PRIOR APPLICATION NUMBER: US 08/227,371 FILING DATE: 14-APRIL-1994 PRIOR APPLICATION NUMBER: US 08/24,915 FILING DATE: 14-APRIL-1994 PRIOR APPLICATION NUMBER: US 08/24,915 FILING DATE: 11-DECEMBER-1993 PRIOR APPLICATION NUMBER: US 07/991,997 FILING DATE: 17-DECEMBER-1993 PRIOR APPLICATION NUMBER: US 07/991,997 FILING DATE: 17-DECEMBER-1992
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08893274
Patent No. 5968821
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                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 156; Conservative
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E Sequence 2, Applic

C Sequence 2, Applic

C Sequence 2, Applic

C Sequence 3, Applic

C Sequence 1, Applic

C Sequence 2, Applic

C Sequence 2, Applic

C Sequence 3, Applic

C Sequence 1, Applic

C Sequence 2, Applic

C Sequence 2, Applic

C Sequence 3, Applic

C Sequence 1, Applic

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US-08-486-047-2
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                                                                                                                                            1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 60
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08480810
Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
                                                                                                                 ò
                                                                                              Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 20005

ZUR: 20005

COMPUTER READALE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATE: US-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
                                                                                                                0; Indels
                                                                                                                                                                                                                                                                    156 AA
                                                                                             Score 1078; DB 2;
Pred. No. 4.93e-85;
                                                                                                                                                                                                            121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                    PRT;
                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08480810
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
                                      : 156 amino acids
amino acid
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                  US-08-480-810-2
                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08486047
Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
CONTRY: USA
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                                                                                                                                                                                                                                                                                                                                                Score 1067; DB 1; Length 156;
Pred. No. 4.84e-84;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
"TILNG PATE: 07-JUN-1995
"TILNG PATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
ENCE 156 AA; 16532 AW; 98534 CN;
                                                                ATTOKABLIANDEN LINGSEN LINGSEN LA REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08486047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                / Match
Local Similarity 98.7%;
hes 154; Conservative
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1 MDPAGGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 156;
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   SOFTWARE: Patentin Release #1.0, Version #1.30
                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORREY/AGENT INFORMATION:
NAME: Inhen, Jeffrey
REGISTRATION NUMBER: 28,957
REEERBOWE: 202-962-4810
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Pred. No. 4.84e-84;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08487033
Patent No. 57390270:
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: MTSIE1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 156 AA: 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08487033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.7%;
Matches 154; Conservative
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Patent No. 5989815
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Canon-Albright, Lisa A.
APPLICANT: Canon-Albright, Lisa A.
TITLE OF INVENTION: GENELINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCE: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER REDABLE FORM:
MEDIUM ITPE: Floppy disk
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                                        PRICK APPLICATION DATE:

PRICK APPLICATION NUMBER: US
PRICK APPLICATION NUMBER: US
PRICK APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRICK APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: INFO: JERRAL OF US 08/214,582
FEFERENCE/DOCKET NUMBER: 24884-109348-B
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8300
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acida
TYPE: amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1067; DB 2;
Pred. No. 4.84e-84;
1; Mismatches 1;
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APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
TENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08848251
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Best Local Similarity 98.7%;
Matches 154; Conservative
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US-08-848-251-2
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E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1067; DB 1; Length 156;
Pred. No. 4.84e-84;
1; Mismatches 1; Indels
                                                                               OFFWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 ADDITATION DAIA:
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                                                                                                              APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
                                                                                                                                                                                                                                        PATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE 156 AA; 16532 MW; 98534 CN;
                                                                  E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
Llarity 98.7%;
Conservative
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                      USA
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nes 154; Conser
                                     COUNTRY: US
ADDRESSEE:
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Matches
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STANDARD;

US-08-508-735-2

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Sequence 2, Application US/08508735

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Sequence 2, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
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Pred. No. 4.84e-84;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/508,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
APPLICATION NUMBER: PCT/US95/03316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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SEQUENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09120130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-962-4848
202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.7%;
Matches 154; Conservative
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US-09-120-130-2
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                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                 STATE:
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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
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Pred. No. 4.84e-84;
1; Mismatches 1; Indels 0; Gaps
                                                                                                                                       Sequence 2, Application US/08474177

Patent No. 5624819

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Candon-Albright, Lisa A.
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/474,177
FLING DATE: 07-JUN-1995
FLING APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FLING DATE: 11-MAR-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: U5 08/251,938
FRICH APPLICATION DATA:
APPLICATION NUMBER: U5 08/215,087
FRILNG DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5 08/215,086
FRILNG DATE: 18-MAR-1994
FRIEDRACK-MAR-1094
ATTORNEY/AGENT INFORMATION:
NAME: THERECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
BRUCE 156 AA; 16532 MW; 98534 CN;
                                                                                                             Sequence 2, Application US/08474177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.7%;
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels 0;
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: WTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 156;
                                                                                                                                                                                                STATE: DC
COMPUTER TEADABLE FORM:
ABDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NAMBER: US/09/120,130
FILING DATE:
CLASSIFICATION: DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/251,938
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
ATTONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,957
REEERRENCE/DOCKET NUMBER: 24,884-109348
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1067; DB 3;
Pred. No. 4.84e-84;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 156 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Best Local Similarity 98.7%;
Matches 154; Conservative
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120 ELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
121 ELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 157
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USA
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PCT-US93-09945-4
                                              JT 14
US-08-589-981-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252
FILING DATE: Not yet assigned
CLASSIFICATION:
                                                                                                                                                   Sequence 5, Application PC/TUS9605252
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: p19: A Cell Cycle Inhibitor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Weber, Ellen L. REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1067; DB 4;
Pred. No. 4.84e-84;
0; Mismatches 0
                                                                                  157
                                   121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..157
OTHER INFORMATION: /note= "human.pl6"
ICE 157 AA; 16674 MW; 100395 CN;
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                  PRT;
                                                                                                                                      Sequence 5, Application PC/TUS9605252
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 157 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
                                                                                                                                                                                                                                                    USA
                                                                        T 13
PCT-US96-05252-5
                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                     XXXXX
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236 MORAAGSSMEDSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIOVMMMGSARVA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ELLLLHGAEPNCADPATLTRPVHDAAREGFILDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                     Sequence 2, Application US/08589981
Patent No. 5672508
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lamphere, Lou
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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 391 AA.
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98.7%; Pred. No. 9.03e-84;
vative 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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ENCE 391 AA; 42306 MW; 652242 CN;
 PRT;
                                                                                                         Sequence 2, Application US/08589981
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STANDARD;
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nes 154; Conservative
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US-09-016-869A-2.rai

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TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09945
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1030; DB 4; Length 148;
Pred. No. 1.05e-80;
0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                   FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-CCT-1992
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                    Sequence 4, Application PC/TUS9309945
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE 148 AA; 15844 MW; 88737 CN;
                                                              Sequence 4, Application PC/TUS9309945
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 148; Conservative
             XXXXX
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129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156

121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148

61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120

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Search completed: Thu Jul 20 08:36:57 2000 Job time: 7 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:35:12 2000; MasPar time 11.77 Seconds 625.481 Million cell updates/sec Run on:

Tabular output not generated.

1 MDPAAGSSMEPSADWLATAA......TRGSNHARIDAAEGPSDIPD 156 >US-09-016-869A-2 (1-156) from US09016869A.pep 1078 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir63 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 43.845; Variance 94.938; scale 0.462

Statistics:

SUMMARIES

| | 10.00 | |
|----------------------------|---|--|
| Pred. No. | 3.86e-175 1.59e-110 1.59e-110 2.46e-911 3.82e-41 1.76e-33 1.75e-32 1.75e-32 1.75e-32 1.75e-32 1.75e-32 1.75e-32 1.75e-32 1.76e-33 | |
| Description | cyclin dependent kina pisiwkab - mouse CDK4 inhibitor pl4(IN pi6INKAb - mouse CDK4/CDK6 inhibitor pcyclin-dependent kina CDK6/CDK6 inhibitor pl8 - CDK4/CDK6 inhibitor pl gene pisiwkab protein ankyrin 1, erythrocyt ankyrin 1, erythrocyt ankyrin 1, erythrocyt ankyrin, erythrocyt ankyrin - mouse ankyrin - mouse ankyrin - mouse ankyrin - ferit diret ankyrin - ferit fily (fily (| |
| DI DI | UE0141 178845 1858445 18583473 18583473 1857373 1857373 1857373 1857373 1857473 187771 1837771 18346 115346 115346 | |
| DB | 00000000000000000000000000000000000000 | |
| a Query Match Length | 156 130 130 164 164 168 168 188 188 188 188 188 188 188 188 | |
| % Query Match | 999.0 677.0 677.0 677.0 677.0 677.0 679.0 | |
| Score | 1067 7229 7229 8633 3341 1344 1174 1173 1160 1160 1160 1160 1160 | |
| Result No. | 22222222222222222222222222222222222222 | |

FRENCE \$39359

#authors Serrano, M.; Beach, D.

#authors Serrano, M.; Beach, D.

#title A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.

#cross-references MuID:94081956

#accession \$39359

REFERENCE #authors #journal #title

#authors Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, W.P.; Forrester, K.; Gerwin, B.; Serrano, M.; Beach, D.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:11045-11049
#title Mutations and altered expression of pi6INK4 in human cancer.
#accession 159268

##status translation not shown; translated from GB/EMBL/DDBJ ##molecule_type DNA ##residues 1-152 ##label RES #tross-references GB:674232; NID:9710467 ##note this report is a correction

Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.; Johnson, B.E.; Skolnick, M.H. Science (1994) 264:436-440

9-34,'V',36-156 ##label SER this sequence has been corrected in reference I59268

##status preliminary ##molecule_type mRNA

##residues

##note #authors

REFERENCE

#journal

I59585

| 24 142 25 141 26 138 | 13.2 13.1 12.8 | 1964 1423 414 | 242 | T09059 I37275 A53950 | notch4 - mouse death-associated prot transcription factor | 2.41e-06 3.35e-06 8.94e-06 |
|---------------------------------|----------------------|---------------------------------------|---------|---|---|----------------------------------|
| 27 136 28 132 | | | 9 77 79 | B47169 T15888 | ankyrin-like repeat p hypothetical protein | 71e-0 18e-0 |
| o 0 | | 40 | N N | S30355 S45306 | C 03 | 1.60e-04 2.20e-04 |
| - | | N | ~ | 878549 | notch3 protein - huma | 5.63e-04 |
| O M | | CAI | ~ ~ | S18188 A56695 | notch protein homolog notch2 protein homolo | 7.68e-04 1.05e-03 |
| 4 | 11.4 | CI | 7 | 542612 | transmembrane protein | 1.05e-03 |
| 'n | • - | | ~ (| A49128 | cell-fate determining | 1.05e-03 |
| ۰, | | A (A | N (1) | A40043 | notch protein rairic | 1.05e-03 |
| ω. | | CAI | Н | A24420 | notch protein - fruit | 1.05e-03 |
| o (| • | • | ~ | B45771 | 2-5A-dependent RNAase | 3.57e-03 |
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| 4 M | | • | ۱ ۵ | B40858 | | 4.84e-03 |
| 4 | | | 7 | 149045 | . 0 | 6.54e-03 |
| S. | | | н | H71274 | 'ari | .84e-0 |
| | | | | ALIGNMENTS | | |
| RESULT 1 | į | ; | | | | |
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| TITLE ALTERNATE_NAMES | 88 | cyclin dependent CDK4 inhibitor pl | tor. | in dependent kinase - human inhibitor p16(INK4A/MTS1); | cyclin-dependent | kinase |
| ORGANISM | # \$0 | rmal_nam | e, | omo sapiens | | |
| DATE | 02- | 02-Jun-1998 #seq 26-Aug-1999 | \$# 666 | equence_rev | ision 10-Jul-1998 #text_change | hange |
| ACCESSIONS | JEO | 141; ISS | 268 | 539359; | I59585; JC5679 | |
| REFERENCE | SEO SEO | | | | | |
| #authors | Hua | Huang, C.G. | | C.G.; Deng, W.; Fu | Fu, J.L. | |
| title | M | ٦ ۲ | cloning | . თ | ng of P161nk4 | cDNA from hela |
| | 0 | | | | | |
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| ##molecule_ | e_type | mRNA | | 1 1 1 1 | | |
| ##residues | 9 | | ## | ##IMDEL HUA | | |
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Chinese J. Biotechnol. (1997) 13:105-107
Chicke J. Biotechnol. (297) 13:05-107
Chicken cloning and sequencing of P16 ink4 cDNA from hela cell.
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Oncogene (1995) 11:635-645
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#title A cell cycle regulator potentially involved in genesis many tumor types.
#cross-references MID:94204645
#accession I59585
                                                                                                                                                                                                                                                                                  p151NK4b
#length 130 #molecular-weight 13788 #checksum 7879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #length 156 #molecular-weight 16532 #checksum 6490
                                                                                                                                                                                                                                                                                                                                                             #gene pl6ink4; MLM; CDKN2; MTS1 ##cross-references GDB:335362; GDB:CDKN2A; OMIM:600160 #map_position 9921-9921 CLASSIFICATION #superfamily unassigned ankyrin repeat proteins KEYWORDS cell cycle control; protein kinase inhibitor; tumor
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Best Local Similarity 98.7%; Pred. No. 3.86e-175;
Matches 154; Conservative 1; Mismatches 1;
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Best Local Similarity 88.3%; Pred. No. 1.59e-110;
Matches 106; Conservative 6; Mismatches 8;
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                                                                                                                          51-152 ##label RE2
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##molecule_type mRNA
##residues 1-19, TP', 22, 24-31, HSW', 35-138 ##label HAN
##cross-references GB:L36844; NID:9556197; PIDN:AAA50282.1; PID:9556198
##experimental_source HaCaT cells
SNCE
                                                                                                                                                                                                                                                                       B55479 #type complete
CDK4 inhibitor p14(INK4B/MTS2) - human
CDK6-associated protein p15(INK4B); cyclin-dependent kinase
inhibitor 2B; multiple tumor suppressor 2
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
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Nature (1994) 371:257-261
p15(INK4B) 1s a potential effector of TGF-beta-induced cell
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Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler,
K.W.; Vogelstein, B.
#journal Cancer Res. (1994) 54:6353-6358
#title Deletion of pl5 genes in brain tumors.
#cross-references WUID:95079408
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                                                                                                                           #authors Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Xiong, Y. Genes Dev. (1994) 8:2939-2952 #title Growth suppression by pl8, a p16(INK4/MTS1)- and p14 (INK4/MTS1)-related CDK6 inhibitor, correlates with wild-type pRb function.
                                                                                           70 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIARYLHAATG 129
16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMGSARVAELLLLHGAEPNCADP 75
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Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III,
Johnson, B.E.; Skohnick, M.H.
Science (1994) 264:436-440
A cell cycle regulator potentially involved in genesis o
many tumor types.
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#length 138 #molecular-weight 14722 #checksum 1236
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#map_position 9p21-9p21
FWORDS cell cycle control; protein kinase inhibitor; tumor
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##residues 1-138 ##label GUA
##cross-references GB:U17075; NID:g639715; PID:g639716
##experimental_source HeLa cells
SNCE 847593
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B55479; S47593; I81183; I52713
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NCE 152713
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##cross-references GB:S75756; NID:g861470
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##residues 53-138 ##label KAM
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1-166 ##label CHA
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Identification of human and mouse pl9, a novel CDK4 and CDK6
inhibitor with homology to pl6(ink4).
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Cloning and characterization of murine p16INK4a and p15INK4b
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C.; Beach, D.; Sherr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLRTATG 137
                                                                   1 MESAADRLARAA-QGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGA 59
                                                     18 LASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSARVAELLLLHGAEPNCADP 77
                                                                                                                                                                                                                #formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 type complete cyclin-dependent kinase inhibitor p19 - human formal_name flow sapiens #common_name man 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change A57378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                p161NK4a
#length 167 #molecular-weight 17870 #checksum 1257
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                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
#fresidues 1-167 *****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 167;
 Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GB:S79251; NID:g1087090; PID:g1087091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 663; DB 2; Length 167
Pred. No. 4.46e-98;
20; Mismatches 14; Indels
                          Indels
Score 725; DB 2; LA Pred. No. 9.09e-110; 6; Mismatches 9;
                                                                                                                                                                                                                                                                                    Quelle, D.E.; Ashmun, R.A.; Hannon,
Trono, D.; Richter, K.H.; Walker,
C.J.; Serrano, M.
                                                                                                                                                                                       158352 #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-164 ##label CHA ##cross-references GB:U20498
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#accession I58352
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Query Match 67.3%;
Best Local Similarity 87.5%;
Matches 105; Conservative
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Local Similarity 72.2%;
les 91; Conservative
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#authors
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Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. Mol. Cell. Blol. (1995) 15:2682-2688
Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to pl6(ink4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Cell. Biol. (1995) 15:2672-2681
Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
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                                                                                                                                                                                                                                         71 TSG-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFLAAES 129
                                                                                                                                                                                                                                                                  #superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology #length 164 #molecular-weight 17352 #checksum 5271
                                                                                                                                                             11 LSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQD 70
                                                                                                                                                                                    9 GDRLSGARARGDVQEVRRLLHRELVHPDALNRFGRTALQVMMFGSPAVALELLKQGASPN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 VQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                             A57379 #type complete
CDK4/CDK6 inhibitor pi9 - mouse
#formal_name Mus musculus #common_name house mouse
08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
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                                                                                  Length 164;
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                                                                              Score 353; DB 2; Length 164
Pred. No. 3.82e-41;
19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 341; DB 2; Length 166
Pred. No. 5.04e-39;
19; Mismatches 39; Indels
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#accession B57378
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                                                                              Query Match 32.7%;
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 1.6%;
Local Similarity 49.6%;
les 59; Conservative
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A57379
                                                                                                                        60; Conservative
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Gaps

Length 168;

SUMMARY

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Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L. Cancer Res. (1995) 55:1607-1612
Association of rat pl51NK4b/pl61NK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal
                                                                Mol. Cell. Biol. (1995) 15:2672-2681
Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
ness MUID:95257948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 PNLKDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVWKLGNPEIARRLLLRGAN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152720 #type fragment
gene pl51NK4B protein - rat (fragment)
#formal_name Rattus sp. #common_name rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ankyrin 2, neuronal long splice form - human ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid ankyrin ankyrin 2, short form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLEHGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
                          Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun,
                                                                                                                                                                                                                                                                                                                                                                  Score 292; DB 2; Length 168
Pred. No. 1.75e-30;
29; Mismatches 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 MAMGSARVAELLLIHGAEPNCADPATLTRPVHDAAREGFLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAMGSAQVAELLILHGAEPNCADPATLTRPVHDAAREGFLD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 284; DB 2;
Pred. No. 4.14e-29;
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##cross-references GB:S77734; NID:g998711
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#length 41 #checksum 3296
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#accession I52720
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Best Local Similarity 43.0%;
Matches 52; Conservative
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Best Local Similarity 97.6%;
Matches 40; Conservative
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##residues 1-4.
                                                                                                                                                         B57379
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ALTERNATE_NAMES
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SUMMARY
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CDK6 inhibitor p18 - human
Cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
Kinase CDK6 inhibitor p18
#formal_name Homo sapiens #common_name man
23.Mar-1995 #sequence_revision 23-Mar-1995 #text_change
##cross-references GB:U20497; NID:g791204; PIDN:AAA85437.1; PID:g791205
FICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology; EGF homology
: #length 166 #molecular-weight 17920 #checksum 3767
                                                                                                                                                         ä
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##residues 1-168 ##label GUA
##cross-references GB:U17074; NID:g639713; PIDN:AAC50074.1; PID:g639714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #gene ##ferross-references GDB:594931
#map_position lp32-1p32
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
KEYWORDS cell cycle control; protein kinase inhibitor; tumor
                                                                                                                                                                                                                       3 EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVWRLGNPEIARRLLLRGAN 62
                                                                                                                                                                                                GDRLSGARPRGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPN 68
                                                                                                                                                                                                                                                                                69 VQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
                                                                                                                                                                                                                                                                                                       10 EPSADWILATAAARGRVEEVRALLEAVALDNAPNSYGRRPIQVMMGSARVAELLILIHGAE 69
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CDK4/CDK6 inhibitor pl8 - mouse
#formal_name Mus musculus #common_name house mouse
08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #fitle Growth suppression by p18, a p16(INK4/MTS1)- and p14 (INK4/MTS4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRb function. #cross-references MUID:95095079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         suppressor
#length 168 #molecular-weight 18127 #checksum 9379
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                                                                                                              Length 166;
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                                                                                                          Score 338; DB 2; Length 166
Pred. No. 1.70e-38;
20; Mismatches 39; Indels
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Pred. No. 7.29e-32;
35; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 LRAAAGGTRGSNHARIDAA 148
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Best Local Similarity 39.6%;
Matches 55; Conservative
                                                                                                        Query Match
Best Local Similarity 48.7%;
Matches 58; Conservative
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A55479
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                      CLASSIFICATION
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Length 41; Indels

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471 AARAGOVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHMAHPDAATTNG 530
                                                                                                                                                                                                                                                                                                                                                                                                               531 YT-PLHISAREGQVDVASVLLEAGAAHSLATKKGFTPLHVAAKYGSLDVAKLLLQRRAAA 589
                                                                                                                                                                                                                                                                                                                                                               20 AAR-GRVEEVRALLEAVALPNAPNSYGRRPIQVM-MMGSARVAELLILHGAEPNCADPAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, W.C.; Ran, Y.W.; Palek, J. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734 CDNA, sequence for human erythrocyte ankyrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ankyrin 1, erythrocyte splice form 3 - human ankyrin 1, erythrocyte splice form 3 - human ankyrin 2.1, erythrocyte; ankyrin-R ankyrin 2.2, erythrocyte
#formal_name Homo sapiens #common_name man 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change B35049
                                                                                                                                                                                                                                   #molecular-weight 430340 #checksum 3664
thomology *label AN11/
thomology *label AN12/
thomology *label AN13/
thomology *label AN14/
thomology *label AN15/
thomology *label AN17/
thomology *label AN17/
thomology *label AN18/
thomology *label AN18/
thomology *label AN20/
thomology *label AN21/
                                                                                                                                                                                                                                                                     Score 181; DB 2; Length 3924;
Pred. No. 3.58e-12;
20; Mismatches 53; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##GENERAL GDB:ANK1; ANK
##GENERAL GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing
                                                   #domain ankyrin repeat he domain ankyrin repeat he domain ankyrin repeat he domain ankyrin repeat he #domain ankyrin repeat he
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#length 3924 #molecular-wei
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Matches 48; Conservative
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##residues 1-185
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J. Gall Biol. (1993) 123:1463-1473
440.kD ankyrinB: structure of the major developmentally
regulated domain and selective localization in unmyelinated
                                                                                                                                                                                                                                #authors Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
#Journal J. Cell Biol. (1991) 114:241-253
#title Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.
#cross_references MUID:91302466
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##residues 463-474,'PE',477-495 ##label TSE
##cross-references GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
NCE A49462
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#title Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
   06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                     S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                      Chan, W.
submitted to the EMBL Data Library, September 1993
S37431
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##cross-references EMBL:226634; NID:9406287; PIDN:CAA81387.1;
PID:9406288
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##residues 1-2077 ##label OTI
##cross-references GB:X56957
ression B39643
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#accession A49462
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ankyrin 1, erythrocyte splice form 2 - human
ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2, erythrocyte
#formal_name Homo sapiens #common_name man
27.401-1990 #sequence_revision 01-oct-1992 #text_change
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#domain ankyrin repeat homology #label AN #label AN #domain ankyrin repeat homology #label AN #label #label AN #label 
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#GENERAL GDB:ANK1; ANK
##CIOSS-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #Superfamily ankyrin; ankyrin repeat homology
REYWORDS alternative splicing; cytoskeleton
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16; Mismatches 50; Indels
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##molecule_type mRNA
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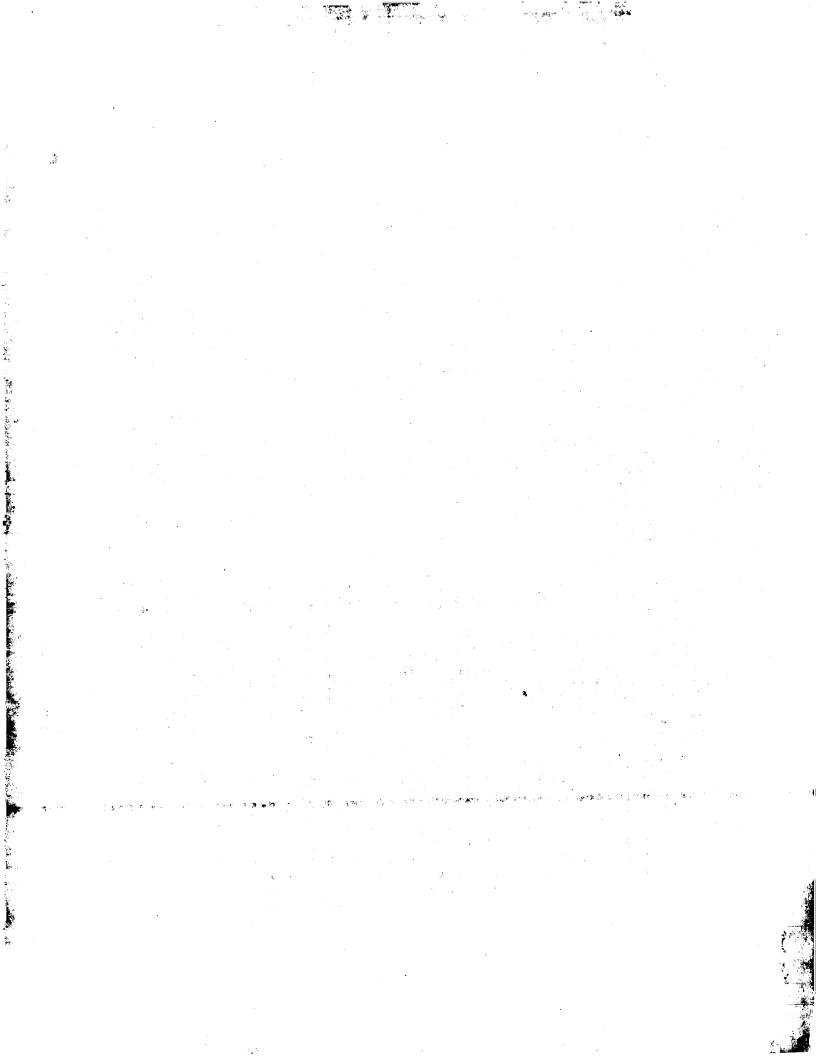
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#authors Hermann, J.; Barel, M.; Frade, R.
#journal Blochem. Bloch
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#journal Nature (1990) 344:36-42
#title Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.
#cross-references MUID:90158830
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#journal J. Biol. Chem. (1990) 265:10589-10596
#title Mapping the binding sites of human erythrocyte ankyrin the anion exchanger and spectrin.
#cross-references MUID:90285190
#domain ankyrin repeat homology #label AN16\
#domain ankyrin repeat homology #label AN17\
#domain ankyrin repeat homology #label AN18\
#domain ankyrin repeat homology #label AN18\
#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN21\
#domain ankyrin repeat homology #label AN21\
#domain ankyrin repeat homology #label AN3
#length 1880 #molecular-weight 20606 #checksum 6968
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##residues 910-929 ##label HER
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Job time : 14 secs.
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Lux, S.E.; Barker, J.E.
J. Biol. Chem. (1993) 268:9533-9540
Complex patterns of sequence variation and multiple 5' and 3'
ends are found among transcripts of the erythroid ankyrin
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                                                                                                                                                        #label MATI\
#product ankyrin 2.2, erythrocyte #status predicted
#label MAT2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 174; DB 1; Length 1881;
Pred. No. 4.30e-11;
16; Mismatches 50; Indels 6; Gaps
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ankyrin, erythrocyte - mouse
#formal_name Mus musculus #common_name house mouse
27-May-1994 #sequence_revision 03-Aug-1995 #text_change
13-Aug-1999
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##molecule_type mRNA
##residues
##cross-references EMBL:X69063; NID:9311816; PIDN:CAA48801.1;
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SUMMARY
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511 LHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG 570
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Pred. No. 6.11e-11;
17; Mismatches 50; Indels 6;
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PID:g311817
#superfamily ankyrin; ankyrin repeat homology
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Best Local Similarity 38.1%;
Matches 45; Conservative
                CLASSIFICATION
KEYWORDS
FEATURE
                                                                       48-80
81-113
114-146
147-175
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Oy 75 PATLIRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLJ
Search completed: Thu Jul 20 08:35:26 2000

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 20 08:35:43 2000; MasPar time 7.46 Seconds 637.235 Million cell updates/sec Tabular output not generated. Run on:

>US-09-016-869A-2 (1-156) from US09016869A.pep 1078 1 MDPAAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 segs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot38 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 44.859; Variance 85.215; scale 0.526

SUMMARIES

| Pred. No. | 1.98e-199 | 6.89e-126 | 5.00e-125 | 5.94e-124 | 9.94e-112 | 5.27e-93 | 3.10e-49 | 1.29e-44 | 1.72e-36 | 6.33e-35 | 3.37e-14 | 3.37e-14 | 5.58e-13 | 8.30e-13 | 8.65e-08 | 1.81e-07 | 1.13e-06 | 1.99e-05 | 4.03e-05 | 8.10e-05 | 1.15e-04 | 1.15e-04 | 1.15e-04 |
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| Description | CYCLIN-DEPENDENT KINAS | ANKYRIN, BRAIN VARIANT | ANKYRIN, BRAIN VARIANT | ANKYRIN R (ANKYRINS 2. | ANKYRIN. | NEUROGENIC LOCUS NOTCH | DEATH-ASSOCIATED PROTE | ANKYRIN HOMOLOG PRECUR | NEUROGENIC LOCUS NOTCH |
| А | CDN2_HUMAN | CDN5_MOUSE | CDN5_HUMAN | CDNS_RAT | CDN2_MOUSE | CDN2_MONDO | CDN7_HUMAN | CDN7_MOUSE | CDN6_HUMAN | CDN6_MOUSE | ANKC_HUMAN | ANKB_HUMAN | ANK1_HUMAN | ANK1_MOUSE | NTC4_MOUSE | DAPK_HUMAN | ANKH_CHRVI | NTC3_MOUSE | NOTC_DROME | NTC1_RAT | NOTC_BRARE | NTC1_HUMAN | NOTC_XENLA |
| angth DB | 156 1 | 130 1 | 138 1 | 130 1 | 167 1 | 171 1 | 166 1 | 166 1 | 168 1 | 168 1 | 1839 1 | 3924 1 | 1880 1 | 1862 1 | 1964 1 | 1431 1 | 323 1 | 2318 1 | 2703 1 | 2531 1 | 2437 1 | 2444 1 | 2524 1 |
| % Query Match Length | 99.0 | 67.6 | 67.3 | 8.99 | 61.5 | 53.3 | 33.8 | 31.6 | 27.8 | 27.1 | 16.8 | 16.8 | 16.1 | 16.0 | 13.3 | 13.1 | 12.6 | 11.9 | 11.7 | 11.5 | 11.4 | 11.4 | 11.4 |
| Score | 1067 | 729 | 725 | 720 | 663 | 575 | 364 | 341 | 300 | 292 | 181 | 181 | 174 | 173 | 143 | 141 | 136 | 128 | 126 | 124 | 123 | 123 | 123 |
| Result No. | -1 | 7 | m | 4 | ഗ | φ | 7 | ω | თ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 50 | 21 | 22 | 23 |

ALIGNMENTS

| SG | LT 1 CDN2_HUMAN STANDARD; PRT; 156 AA. |
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| 5 5 | UI-NOV-1995 (Rel. 32, Created) |
| | 15-JUL-1999 (Rel. 38. Last annotation undate) |
| | CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (P16-INK4A) |
| DE | |
| GN | CDKN2A OR CDKN2. |
| SO | \sim |
| 8 | Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; |
| 8 | |
| RN | |
| RP | |
| X | MEDLINE; 94081956. |
| RA | |
| RT | "A new regulatory motif in cell-cycle control causing specific |
| RT | inhibition of cyclin D/CDK4."; |
| RL | Nature 366:704-707(1993). |
| RN | |
| RP | SEQUENCE OF 51-152 FROM N.A. |
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| í | 0.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 |
| £ £ | SACINITION MISS. |
| 2 7 | A cert cycle regulator potentially involved in genesis of many tumor |
| KI | types."; |
| R. | Science 264:436-440(1994). |
| RN | |
| ЯP | |
| X | MEDLINE; 96182088. |
| æ | Smith R., Parry D., Tahara H., Stone S., Peters |
| RŢ | "Regulation of p16CDKN2 expression and its implications for cell |
| RT | immortalization and senescence."; |
| RL | Mol. Cell. Biol. 16:859-867(1996). |
| RN | [4] |
| RP | X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6. |
| XX. | MEDLINE: 98421670. |
| RA | Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Payletich N.P.: |
| RT | "Structural basis for inhibition of the cyclin-dependent kinase Cdk6 |
| E | by the tumour suppressor pleingla.": |
| 12 | Nature 395:237-243(1998). |
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| 0 | PEUTEW ON MELANOMA VARIANTS |
| Xd | MEDITARE OF STATE |
| 1 5 | 11111111111 |
| ¥ ¦ | Dracopoli N.C., Fountain J.W.; |
| KI | "CDKNZ mutations in melanoma."; |

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CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
MEDLINE; 95375774.
                                                                                                                    MEDIJINE; 94338359.

Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;

"Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
(cyclin-dependent kinase-4 inhibitor) gene in human primary non-small cell lung carcinomas.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.; "Mutations in the pigink4/MTSJ/CDKN2, pi5ink4B/MTS2, and pl8 genes primary and metastatic lung cancer."; Cancer Res. 55:1448-1451(1995).
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MEDLINE; 97472457.
                                                                                                                                                                                                                                                                                                                                                                       "The MTS1 gene is frequently mutated in primary human esophageal
                                                                                                                                                                                                                                                                                                               VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
MEDLINE; 95060835.
Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
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Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mutations associated with familial melanoma impair p16INK4
                                                 Smith-Soerensen B., Hovig E.; "CDKNZA (p16INK4A) somatic and germline mutations."; Hum. Mutat. 7:294-303(1996).
                                                                                                                                                                           cell lung carcinomas.";
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                                                                                                           VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
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Cancer Surv. 26:115-132(1996).
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                         REVIEW ON VARIANTS.
MEDLINE; 96303699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.; "Novel germline pi6ink4 allele (Aspl45Cys) in a family with multiple
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Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
"Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France.";
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/ A -> P (IN A LUNG TUMOR AND MELANOMA).

/ A -> S (IN A BILIARY TRACT TUMOR).

/ FTId=VAR_001411.

G -> D (IN A PANCREAS TUMOR).

/FTId=VAR_001412.
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/FILG-VAR_001408.
L -> P (IN A BILIARY TRACT TUMOR AND FAMILIAL MELANOWA).
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Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz. A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
Hum. Mol. Genet. 7:941-941(1998).
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Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
Polymorphism; 3D-structure.
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                                                                                                                                                                                                                                      Hum. Mol. Genet. 7:209-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic carcinomas.";
Hum. Mutat. 12:70-70(1998).
FAMILIAL MELANOMA. 98087572.
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DOMAIN 12
REPEAT 13
        VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95380169.

Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
"Cloning and characterization of murine plcink4a and pl5ink4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBLIBARITY: HET-FRODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-!- INDUCTION: BY TGF-BETA.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alterations in murine primary T-cell lymphomas.";
Oncogene 14:1361-1370(1997).
-1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
POTENTIAL BFPECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                       61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malumbres M., de Castro I., Santos J., Melendez B., Mangues R., Berrandez-Tiquerasa J.; Mangues R., "Inactivation of the cyclin-dependent kinase inhibitor pi5iNK4b by deletion and de novo methylation with independence of pi6iNK4a
                                               E -> D (IN A BILIARY TRACT TUMOR).
/FIIG-VAR_001415.
/FIIG-VAR_001416.
E -> D (IN A BILIARY TRACT TUMOR).
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 -> P (IN FAMILIAL MELANOMA AND
                                                                                                                                                                                               Length 156;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                         Score 1067; DB 1; I
Pred. No. 1.98e-199;
1; Mismatches 1;
                MELANOMA).
/FTId-VAR_001414
                                                                                                                                                                                                                                                                                                                                                                                                         121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                             121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AA.
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Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                           Match 199.0%;
Local Similarity 98.7%;
les 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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STRAIN-C57BL/6J X DBA;
MEDLINE; 97322242.
24
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24
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P55271;
                                                                                                                                                                                           Query Match
VARIANT
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                                                                                        VARIANT
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Matches
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Matera G.A., Xiong Y.;
"Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
CDK6 Inhibitor, correlates with wild-type pRb function.";
Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 ATLIRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIARYLHAATG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'A cell cycle regulator potentially involved in genesis of many tumor
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
PADLINE, 94359611

Hannon G.J., Beach D.;
PplSINK4B is a potential effector of TGF-beta-induced cell cycle
                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYCLIN-DEPENDENT KIRASE 4 INHIBITOR B (P14-INK4B)
(MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harshman K.,
                                                                                                                              Length 130;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94204645.
Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
Skolnick M.H.;
                                                        Repeat; ANK repeat.
2 X ANK MOTTE REPEATS.
ANK MOTTE 1 (INCOMPLETE).
ANK MOTTE 2.
WHY MOTTE 7.
                                                                                                                          Score 729; DB 1; Le
Pred. No. 6.89e-126;
6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
MEDLINE; 95188190.
                                                                                                                                                                                                                                                                                              138 AA
                                                                                                                                                                                                                                                                                              PRT;
         EMBL; U66085; AAB39833.1; -. EMBL; U66084; AAB39833.1; JOINED
                                                                                        65 95 A
130 AA; 13788 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 53-138 FROM N.A.
                                                                                                                            Match 67.6%;
Local Similarity 88.3%;
les 106; Conservative
                                                         Cell cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 264:436-440(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 371:257-261(1994).
                               MGD; MGI:104737; CDKNZB.
PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 95095079.
                                                                                                                                                                                                                                                                                                                                                                              CDKN2B OR MTS2
                                                                                                                                                                                                                                                                                  CDN5_HUMAN
P42772;
                                                                                                    SEQUENCE
                                                                                                                              Query Match
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                                                                               REPEAT
                                                                   DOMAIN
                                                                                          REPEAT
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                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation—
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SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLRTATG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSARVAELLLLHGAEPNCADP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Association of rat pi5inK48/pi6inK4 deletions with monosomy 5 in
kidney epithelial cell lines but not primary renal tumors.";
Cancer Res. 55:1607-1612(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
-i- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEDURENCE FACE.
MEDLINE; 96001392.
HINO O., KODAYASHI E., Hirayama Y., KoDAYASHI T., Kubo Y.,
TSuchiya H., Kikuchi Y., Mitani H.;
"Molecular genetic basis of renal carcinogenesis in the Eker rat
""And of tuberous sclerosis (TSC2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat: ANK repeat: Disease mutation. 2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> E (IN LUNG ADENOCARCINOMA).
/FIId=VAR_001489.
/FIId=VAR_001489.
SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
OLL -> HSW (IN REF. 2).
WHY (IN REF. 2).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 725; DB 1; Length 138;
Pred. No. 5.00e-125;
6; Mismatches 9; Indels
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                                                                   SIMILARITY: CONTAINS 2 ANK REPEATS.
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EMBL; L36844; AAA50282.1; -.
EMBL; S69805; AAD14049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 46-86 FROM N.A. MEDLINE; 95228036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 67.3%;
Local Similarity 87.5%;
les 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39
103
47
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23
32
138 AA;
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DD CONS_RAT

DT 01-0CT-199

DT 01-0CT-199

DT 15-DEC-199

DE CYCLIN-DEI

GN RATHUS NOI

COC EURARYOCLA,

COC EURARYOCLA,

RA MEDLINE;

RA TSUCHINE;

RA MEDLINE;

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CONFLICT
SEQUENCE
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SOUTH THE TENT THE TEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                  -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN TESTIE, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
-1- SIMILARITY: BELONGS TO THE CDKNS FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; "Cloning and characterization of murine piginK4a and pi5iNK4b genes."; Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBGNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES , CONTAINED CDK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATLTRPVHDAAREGFLDTLMVLHKAGARLDVCDAWGRLPVDLAEEQGHRDIARYLHAATG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIEFRATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATAAARGQVETVRQLLEAGADPNAVNRFGRRPIQVMMGSAQVAELLLLHGAEPNCADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
AC45B21FA69FAD92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHORT FORM.
FOR THE SHORT FORM.
2 X ANK MOTIF REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 720; DB 1; L
Pred. No. 5.94e-124;
8; Mismatches 8;
INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AA.
                                                                                                                                    -! - SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LONG FORM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
95
31
95
95
13748 MW;
                                                                                                                                                                                                                                                                                                                                                           EMBL; S79760; AAB35360.1; -. EMBL; S77734; CAB33639.1; -. PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 66.8%;
Local Similarity 86.7%;
Nes 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
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5
5
65
130 AA;
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SEQUENCE FROM N.A.
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                                                                                                                 INHIBITORS.
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P51480;
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SEQUENCE
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PFAM; PF00023;
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Sherburn T.E., Gale J.M., Ley R.D.;
Sherburn T.E., Gale J.M., Ley R.D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATON OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
-!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INTIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                              Repeat; ANK repeat; Alternative initiation.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MESAADRLARAA-QGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                    9 MEDSADWILATAAARGRVEEVRALILEAVALPNAPNSYGRRPIQVWMGSARVAELLLIHGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (THOMA)
(TUMOR SUPPRESSOR CDRN2A).
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
                                                                                                                                                                                                                                                                                                                                             Score 663; DB 1; Length 167;
Pred. No. 9.94e-112;
20; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                           MISSING (IN SHORT ISOFORM).
88C4588A105ECB8F CRC64;
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                                                                                                                                                                                                                                                                                                           167 AA; 17870 MW;
                                                                                                                                   EMBL; L76150; AAA85453.1; -.
MGD; MGI:104738; CDKN2A.
PFAM; PF00023; ank; 2.
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.2%;
Matches 91; Conservative
                                                                                                                                                                                       Cell cycle; Anti-oncogene;
DOMAIN 4 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                           34
66
100
152
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68
101
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077617;
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REPEAT
REPEAT
VARSPLIC
SEQUENCE
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(epeat; ANK repeat; Alternative initiation. 4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J., Lahkil J.M., Sherr C.J., Downing J.R., "Molecular cloning, expression pattern, and chromosomal localization of human CDKN2D/INK44, an inhibitor of cyclin D-dependent kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guan K.L., Jenkins C.W., Li Y., O'Reefe C.L., Noh S., Wu X., Zariwala M., Matera A.G., Xiong Y.; "Isolation and characterization of pl9INK4d, a pl6-related inhibitor specific to CDK6 and CDK4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98421670.
Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Payletich N.P.;
"Structural basis for inhibition of the cyclin-dependent kinase Cdk6
by the tumour suppressor pl6INK4a.";
Nature 395:237-243(1998).
                                                                                                                                                                                                                                                        12 SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMMGSARVAELLLIHGAEPN 71
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutation testing in melanoma families: INK4A, CDK4 and INK4D."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to p16ink4 "; Mon. Belo. 1810. 18:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
                                                                                                                                                                       Length 171;
                                                                                                                                                                     Score 575; DB 1; Length 171
Pred. No. 5.27e-93;
15; Mismatches 22; Indels
                                                                                                                        MISSING (IN SHORT ISOFORM).
MW; 694264F5D0F4F6CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    CENT_HUMAN STANDARD; PRT; 166 AA. P55273; 013102; 010-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                        Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Biol. Cell 7:57-70(1996).
                                                                                                                                                                       53.38;
                    Cell cycle; Anti-oncogene;
DOMAIN 46 169
                                                                                                                                                                                     larity 69.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 29:623-630(1995).
                                                                                                                                      18707
                                                                   109
143
169
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TISSUE-BONE MARROW;
MEDLINE; 96121373.
                                                                                                                                      171 AA;
                                                                                                                                                                                      Local Similarity
hes 83; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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46
1111
144
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US-09-016-869A-2.rsp

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cyclin D-dependent kinases CDK4 and CDK6.";
Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                      MEDLINE; 98013176
                                                                                                [3]
STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDN6_HUMAN
P42773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                        Holak T.A.;
"Structure of human cyclin-dependent kinase inhibitor p19(INK4d):
"Structure of human ankyrin-repeat-containing structures and
implications for the dysfunction of tumor suppressor p16(INK4a).";
Structure 6:1279-1290(1998).
-i- FUNCTION: INPERACTS STRONGLY WITH CDK4 AND CDK6.
-i- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVQDTSG-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFL 126
                               Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AGDRISGAAARGDVQEVRRILHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.; "Novel INK4 proteins, pl9 and pl8, are specific inhibitors of the
                                                                                                                                                                                                                                                                                                   A X ANK MOTIF REPEATS.

ANK MOTIF 1.

ANK MOTIF 2.

ANK MOTIF 3.

ANK MOTIF 3.

ANK MOTIF 4.
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Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 364; DB 1; Length 166;
Pred. No. 3.10e-49;
22; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                             -> P (IN REF. 3).
2FACD11CF56340DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDN7_MOUSE STANDARD; PRT; 166 AA. Q60773; Q60794; Q1-NOY-1997 (Rel. 35, Last sequence update) 01-NOY-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                               -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
          X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE; 98455510.
                                                                                                                                                                                                                                     EMBL; U49399; AAB03772.1; -.
EMBL; U40343; AAB18139.1; -.
EMBL; U20499; AAA85436.1; -.
EMBL; AF061327; AAC27450.1; -.
PDB; 1B18; 16-FEB-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                           33.8%; silarity 49.2%; EConservative
                                                                                                                                                                                                                                                                                                                  PFAM; PF00023; ank; 3.
Cell cycle; Anti-oncogene;
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137
159
17700 N
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STRAIN-C57BL KAPLAN;
MEDLINE; 95257948.
                                                                                                                                                                                                                                                                                                                                                                                 105
159
166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 61; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AAES 130
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                                                                                                                                                                                                                                                                                                        MIM; 600927;
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                                                                                                                                                                                                                                                                                                     9 GDRLSGARARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (P18-INK4C).
CDKN2C OR CDKN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 95095079.
Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
                                                                                                                                                                                                                                                  Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D., Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
SEQUENCE FROM N.A.
MEDLINE; 95257949.
Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
"Identification of human and mouse pl9, a novel CDK4 and CDK6
inhibitor with homology to pi6ink4.";
Mol. Cell. Biol. 15:2682-2688(1995).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure. DOMAIN 7 137 4 X ANK MOTIF REPEATS. REPEAT 7 41 ANK MOTIF 1.
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Pred. No. 1.29e-44;
19; Mismatches 39; Indels
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ANK MOTIF 3.
ANK MOTIF 4.
ANK MOTIF 4.
A -> P (IN REF. 2).
W; 9E74F5C23B7EBCB2 CRC64;
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73 104 AN
105 137 AN
17 17 AN
166 AA; 17894 MW;
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Best Local Similarity 49.6%;
Matches 59; Conservative
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MGD; MGI:105387; CDKN2D.
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                                                                                                                                                                                                                                                                                                                                                      FOUND IN PANCREAS AND HEART.
--- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
--- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                           Venkataramani R., Swaminathan K., Marmorstein R.; "Crystal structure of the CDK4/6 inhibitory protein pl81NK4c provides insights into ankyrin-like repeat structure/function and tumor-derived pl61NK4 mutations."; Nat. Struct. Biol. 5:74-81(1998).
         "Growth suppression by pl8, a pl6INK4/MTS1- and pl4INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> P (IN BREAST CANCER; LOSS OF CDK6 INTERACTION).
                                                                                                                                                                                                                                                                                                                      MEDLINE; 99175088.
Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T.,
Isai M.-D.;
                                                                                     Blais A., Labrie Y., Poullot F., Lachance Y., Labrie C.;
Structure of the gene encoding the human cyclin-dependent kinase
inhibitor p18 and mutational analysis in breast cancer.";
Biochem. Biophys. Res. Commun. 247:146-153(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disease mutation; 3D-structure
                                                                                                                                                       MEDLINE; 96438606.
Lapointe J., Lachance Y., Labrie Y., Labrie C.;
"A p18 mutant defective in CDK6 binding in human breast cancer
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_001490.
5D66AFA715186E9A CRC64;
                                                     SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 3.
ANK MOTIF 4.
                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS). MEDLINE; 98100086.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF041248; AAC39782.1; -.
EMBL; AF041250; AAC39783.1; -.
EMBL; AF041249; AAC39783.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat;
                                                                                                                                                                                                 Cancer Res. 56:4586-4589(1996).
                                                                                                                                            VARIANT BREAST CANCER PRO-72.
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36
68
101
135
72
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PDB; 1BU9; PRELIMINARY.
 Matera G.A., Xiong Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00023; ank; 3
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                                                                         MEDLINE; 98300299.
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                                                                 TISSUE-BREAST
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REPEAT
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18127 MW;

168 AA;

SEQUENCE

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"Novel INK4 proteins, p19 and p18, are specific inhibitors of the
cyclin D-dependent kinases CDK4 and CDK6.";
MOI. Cell. B101. 15:2672-2681(1995).
-I- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
-I- SUBUNT: HETERRODIMER OF P18 WITH CDK6 (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                         70 PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 129
                                                                                                                                                                                                                            63 PDLKDRTGFA-VIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAREGHLRVVEF 121
                                                                                                                             62
                                                                                                                                                          10 EPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGAE 69
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                                                                              Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                          Length 168;
                                                                         35; Mismatches 48; Indels
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ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
W; BC88D5489307E128 CRC64;
                          Score 300; DB 1;
Pred. No. 1.72e-36;
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36 ANI
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18066 MW; E
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MGD; MGI:105388; CDKN2C.
PFAM; PF00023; ank; 3.
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                          27.8%;
39.6%;
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Query Match
Best Local Similarity 39.6%;
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MEDLINE; 95257948.
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168 AA;
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Matches 52; Conser
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CDN6_MOUSE
Q60772:
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DOMAIN
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"I Genomics 10:858-66(1991).

"I Genomics 10:858-86(1991).

"I GENOMICS 10:858-86(1991).

"I GENOTION: ANEXTRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-SKELETAL ELEMENTS; THEY BIND TO THE ENTHROCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROPEINS TO DELNIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMYC DOMAIN OF THE ERYTHROCYTES AND EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

"I HE CYTOPLASMYC DOMAIN OF THE ERYTHROCYTES AND EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

"I ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY ALTERNATIVE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROGHOUT THE BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNLKDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92009921.
Tae W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                      human brain
genes.";
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           ANC_BUMAN STANDARD; PRT; 1839 AA.
ANC_BUMAN STANDARD; PRT; 1839 AA.
001.405;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 32, Last aequence update)
ANCYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
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ANK MOTIF 1.
ANK MOTIF 2.
                                                                                                                                                                                                                                                                                                         Otto E., Kunimoto M., McLaughlin T., Bennett V.;
Isolation and characterization of cDNAs encoding
ankyrins reveal a family of alternatively spliced
J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PSS0017; DEATH_DOMAIN; 1.
PFAM; PF00023; ank; 22.
PFAM; PF00531; death; 1.
PFAM; PF00791; 2US; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M37123; AAA62828.1; -... S14569; S14569. B14569; B34643; B39643; B39643; MHSSP; Q00420; IAWC.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 463-495 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X56958; G29491; -.
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95
128
                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                   TISSUE-BRAIN STEM;
MEDLINE; 91302466.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                              (FRAGMENT).
                                              122 L 122
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TISSUE-BRAIN STEM.

MEDLINE; 91302466.

Otto E., Kunimoto M., McLaughlin T., Bennett V.;

Isolation and characterization of cDNAs encoding human brain ankytins reveal a family of alternatively spliced genes.";

J. Cell Biol. 114:241-253(1991).

-!- FONCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN SKELETAL ELEMENTS. TO THE LYMPHOCYTE MEMBRANE PROTEIN GPBS, AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AARAGOVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHMAHPDAATTNG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 YT-PLHISAREGQYDVASVLLEAGAAHSLATKKGFTPLHVAAKYGSLDVAKLLLQRRAAA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AAR-GRVEEVRALLEAVALPNAPNSYGRRPIQVM-MMGSARVAELLLILHGAEPNCADPAT 77
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MEDLINE; 94075409.
Chan W., Kordell E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyellnated axons.";
J. Cell Biol. 123:1463-1473(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 181; DB 1; Length 183
Pred. No. 3.37e-14;
20; Mismatches 53; Indels
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ANK MOTIF 3.

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ANK MOTIF 22.

BEATH DOMAIN.

GO -> PE (IN REF. 2).
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nes 48; Conservative
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  Homo sapiens (Human)
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ANKB_HUMAN
Q01484;
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                                                                                                          CELLS THROUGHOUT THE BRAIN.
PIM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 24 ANK REPEATS.
DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

ALTERNATIVE PRODUCTS: THO BRAIN VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING OF GENE ANK2.

IISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
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ANK MOTIF 11.

ANK MOTIF 11.

ANK MOTIF 12.

ANK MOTIF 13.

ANK MOTIF 14.

ANK MOTIF 15.

ANK MOTIF 19.

ANK MOTIF 19.

ANK MOTIF 19.

ANK MOTIF 19.

ANK MOTIF 20.

ANK MOTIF 21.

REPEAT A.

                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSEP G00420; ADDEST BEATH DOMAIN; 1.

MIM; 106410; -.

PROSITE; PS50017; DEATH DOMAIN; 1.

PFAM; PF00023; ank; 22.

PFAM; PF00791; 205; 1.

Cytoskeleton; Alternative splicing; Repeat; ANK repeat;

Phosphorylation; Multigene family.

REPEAT 63 95 ANK MOTIF REPEATS.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z26634; CAA81387.1; -. EMBL; X56957; CAA40278.1; -. PIR; S14533; S14533.
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A REDLINE; 96225450.

A REDLINE; 96225450.

A Gallagher P.G., Schroeter W., Porget B.G., Lux S.E.;

Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

"Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";

INAL. Genet. 13:214-218(1996).

-!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL ELEMPATS; IND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO NA-K ATPASE, TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO NA-K ATPASE, TO THE LIMPHCYTE MEMBRANE PROTEIN BAND 4.2, TO STOSKELETAL PROTEINS ALORIN, TUBULIN, VIMENTIN AND DESMIN.

C CYTOSKELETAL PROTEINS ALSO LINK SPECTRAN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN);

THEY RETAIN MOST OR ALLO F THESE BINDING FUNCTIONS.

C -1- SUBSCHLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
                                                                                                                                                                        471 AARAGQVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHMAHPDAATING 530
                                                                                                                                                   531 YT-PLHISAREGQVDVASVLLEAGAAHSLATKKGFTPLHVAAKYGSLDVAKLLLQRRAAA 589
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                                                                                                LUX S.E., John K.M., Bennett V.; "Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: ACYLATED BY PALMITIC ACID GROUP(S).

DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (HS).

SIMILARITY: CONTAINS 24 ANK REPEATS.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D., Cheung M.C., Kan Y.W., Palek J.; "cDNA sequence for human erythrocyte ankyrin."; Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Length 3924;
                   Pred. No. 3.37e-14;
20; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
TISSUE-HEMATOPOIETIC;
MEDLINE; 90158830.
                                                                                                                                                                                                                                                                                                                                             1880 AA.
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Query Match
Best Local Similarity 38.1%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  control proteins.";
Nature 344:36-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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ANK1_HUMAN
P16157;
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TVEGPLEDPSELEVDIDYFWKHSKDHTSTPNP -> ELRGS
GLQPDLIEGRKGAQIVKRASLKRGKQ (IN A THIRD
                                                                                                                                                             PFAM; PF00033; ank; 22.
PFAM; PF00531; death; 1.
PFAM; PF00791; Jost 1.
PFAM; PF00791; ZUS; 1.
PFAM; PF00791; ZUS; 1.
Phosphorylation; Lipoprotein; Multigene family; Disease mutation; Biliptocytosis; Polymorphism.
                                                                                                                                                                                                                                                                   89 KD DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).
                                                                                                                                                                                                                                                                                                                     55 KD REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
24 X ANK MOTIF REPEATS.
                                                                                                                                                                                                                                                                                              62 KD DOMAIN (SPECTRIN BINDING
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V -> I (IN HS).

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R -> H (IN BRUEGEN).

/FTId=VAR_000597.
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                                                                                                               PIR; S08275; SJHUK.
PIR; A35049; A35049.
PIR; B2500420; IAWC.
MIM; 182900; PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                       EMBL; X16609; CAA34610.1; -.
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R EMBL; M84756; AAAS...

R HSSP; Q00420; IAWC...

DR PROSTE; PS50017; DEATH_DOMAIN; 1.

DR PFAM; PF00023; ank; 23.

DR PFAM; PF00731; death; 1.

DR PFAM; PF00791; 2U5; 11.

DR PFAM; PF00791; 2U5; 11.

RW Cytoskeleton; Repeat; Phosphorylation; Lipoprotein.

RW Cytoskeleton; 1 897 BJRDING DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).

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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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--- SIMILARITY: CONTAINS 22 ANK REPEATS.
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Pred. No. 5.58e-13;
16; Mismatches 50; Indels
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W; 1C5F5E7EFD1CD428 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
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TISSUE-LUNG, AND TESTIS;
MEDLINE; 96281668.
Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
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MEDLINE; 97294559.
Gallahan D., Callahan R.;
the mouse mammary tumor associated gene INT3 is a unique member of the NOTCH gene family (NOTCH4).";
Oncogene 14:1883-1890(1997).
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MEDLINE; 92194507.
RObbins J., Blondel B.J., Gallahan D., Callahan R.;
"Mouse mammary tumor gene int 3: a member of the notch gene family transforms mammary epithelial cells.";
J. virol. 66:2594-2599(1992).
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

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Title: Description: Perfect Score: Sequence:

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PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

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1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 43.910; Variance 82.660; scale 0.531 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| . No. | 1.35e-115 2.59e-115 2.59e-116 1.66e-90 4.38e-92 3.76e-96 3.76e-96 3.76e-96 7.76e-96 7.76e-17 7.63e-43 7.63e-43 7.63e-17 7.63e-13 | |
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| ANKYRIN 3 (ANKYRIN G) 270 KDA ANKYRIN G ISOF | 6 | CYCLIN-DEPENDENT KINAS | NOTCH4 (FRAGMENT). | NOTCH4. | NOTCH4. | K12C11.4 PROTEIN. | UNC-44 (FRAGMENT). | E. ELEGANS ANKYRIN-REL | C. ELEGANS ANKYRIN-REL | C. ELEGANS ANKYRIN-REL | C. ELEGANS ANKYRIN-REL | UNC-44 ANKYRINS. | ANKYRIN G119. | ALTERNATIVE SPLICED FO | ANKYRIN. | HYPOTHETICAL 92.9 KD P | DJ20208.1 (NOVEL RAT E | ESPIN. | TRF1-INTERACTING ANKYR | SIMILAR TO MOUSE INT-3 | NOTCH4. | KIAA0379 (FRAGMENT). | ANKYRIN REPEAT-CONTAIN |
| Q61307 070511 | 012955 | 0921C0 | 099458 | 099940 | 908000 | 044997 | 017344 | 017487 | 017488 | 017486 | 017489 | 017343 | 013484 | 015125 | 024241 | 09Y2V6 | Q9Y544 | 063618 | 095271 | 062390 | 035442 | 015084 | Q9WV72 |
| 11 | 4 | 11 | 4 | 4 | 7 | Ŋ | Ŋ | ß | ស | ហ | Ŋ | S | 4 | 4 | 'n | 4 | 4 | Ħ | 4 | 1 | : | 4 | 1 |
| 1943 | 4377 | 44 | 1095 | 1999 | 2003 | 1435 | 1786 | 1809 | 1815 | 1867 | 2039 | 6994 | 1088 | 78 | 1549 | 832 | 745 | 837 | 1327 | 554 | 1964 | 882 | 525 |
| 15.8 | 15.3 | 15.1 | 15.0 | 15.0 | 15.0 | 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | 14.4 | 14.2 | 14.1 | 13.8 | 13.7 | 13.5 | 13.5 | 13.2 | 13.2 | 13.0 | 12.8 |
| 170 | 165 | 163 | 162 | 162 | 162 | 160 | 160 | 160 | 160 | 160 | 160 | 160 | 155 | 153 | 152 | 149 | 148 | 146 | 146 | 142 | 142 | 140 | 138 |
| 21 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
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Best Local Similarity
Matches 92; Conserv
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089088
089088;
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                                                                                                                                                                                                                HERZOG C.R., YOU M.;
Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-42 FROM N.A.
STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLE/EI AND MUS MUS WUSCULUS;
SANTOS J., MALENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-POUGRAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                        ZHANG S., RAMSAY E.S., MOCK B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding pl6INK4a and pl9ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLOFF E.V., HEREOG C.R., YOU M.; The 5'-flanking region of the El alpha form of the murine pl6INK4a
                                                                                                                                                                                                                                                                         SEQUENCE OF 1-155 FROM N.A.
STRAIN-GS7BL/6J X DBA;
MALUMBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES R.,
SERRANO M., PELLICER A., FERNANDEZ-PIOUERAS J.;
SUDMITTED (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In mouse inbred strains.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: AFC04436; AAC08063.1; -.
EMBL: U49280; AAC00052.1; -.
EMBL: U66087; AAB39600.1; -.
EMBL: U66086; AAB39600.1; -.
EMBL: AFC04588; AAB39600.1; -.
EMBL: U47018; AAC52987.1; -.
EMBL: U47018; AAC52987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-42 FROM N.A.
STRAIN-DBA/2 AND C57BL/6;
GRESSANI W., ROLLINS L.A., MILLER M.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
  (P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN)
                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89AD5E62 CRC32;
              CDKN2A OR ELALPHA OR P16INK4A OR CDKN2A.
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                                                                     SEQUENCE FROM N.A.
STRAIN-DBA/2N; TISSUE-SPLEEN;
MEDLINE; 98151529.
                                                                                                                                                                                                                                                  Mamm. Genome 8:65-66(1997).
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                                                                                                                                                                               SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-11 FROM N.A.
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P42771: 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD00223.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:104738; Cdkn2a.
                                                                                                                                                                                         STRAIN-VARIOUS STRAINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sene 180:213-215(1996).
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                        Mus musculus (Mouse)
                                                                                                                                                                                                      MEDLINE: 97179476
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                                                                                                                                                                                                                                        suppressor gene.
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SEQUENCE
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Length 168;

DB 11;

62.9%; Score 678;

Query Match

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"Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                     CYCLIN DEPENDENT KINASE INHIBITOR PIGINK4A (PIGINK4A TUMOR SUPPRESSOR PROFILM) (CYCLIN-DEPENDENT KINASE INHIBITOR PIGINK4A (PIGINK4A TUMOR SUPPRESSOR CDKNZA OR ELALPHA OR PIG.

MUS musculus (Mouse).

Eukaryota; Metaron.
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                                                                                                                                                                                         SEQUENCE OF 1-42 FROM N.A.
STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERS J.;
"Comparative analysis of the pi6(INK4a) and pi5(INK4b) DNA sequences in mouse inbred strains.";
"Cummitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044335; AAC08962.1;
EMBL; U49279; AAC08051.1;
EMBL; U79229; AAD00224.1;
                                                                                             ZHANG S., RAMSAY E.S., MOCK B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19AFF, is a candidate for the plasmacytoma susceptibility locus, print ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 MEPSADWILATAAARGRVEEVRALLEAVALPINAPNSYGRRPIQVMMGSARVAELLLIHGA 68
                                                                       1 MESAADRLARAAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGA 60
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                           Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 3.53e-116;
20; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
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STRAIN-BALB/CANPT; TISSUE-SPLEEN;
MEDLINE; 98151529.
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  73.0%;
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les 91; Conservative
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111 GRLPVDLAEELGHRDVARYLRAAAG 135
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ID Q9Z1C1
AC Q9Z1C1;
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ID 054846
AC 054846;
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OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGARI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
"Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010807; BAA33540.1;
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OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGARI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
"Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKNZA)
and p15(MTS2/CDKNZB).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010808; BAA33541.1;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
p15/MTS2/CDKN2B (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P16/CDKN2A/MTSI (FRAGMENT).
Fells silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Carnivora; Fissipedia; Felidae; Felis.
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Pred. No. 1.66e-98;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 621; DB 6; Le
Pred. No. 7.07e-104;
8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GRLPVDLAEERGHRDIVRYLRARTGGTGSGSHTGTDGAEG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 AA; 10824 MW; 8C3094E9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 86 AA; 9340 MW; 8C5D01AO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 AA.
                                                                                                                                                                                                                                      102 AA
                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GRLPVDLAEERGHRDVARYLRAAAG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.3%;
97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 86.0%;
Matches 86; Conservative
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Matches 83; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
121 YLRSAG 126
                                                                       129 YLRAAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
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Q9XS51;
Q9XS51;
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Q9XS52;
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SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
FELMANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains ";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79637; AAD0237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VMMMGSAQVAELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VIMMGSAQVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mus.
                                                                                                                                                                                    Mammalla;
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Pred. No. 4.38e-92;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 557; DB 11; Length 86;
Pred. No. 3.66e-90;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TIEMBLREI. 06, Created)
01-JUN-1998 (TIEMBLREI. 06, Last sequence update)
01-NUV-1998 (TIEMBLREI. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                         01-MAY-1999 (TrEMBLrel. 10, Created)
U-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                           Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D5811BE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEC97F63 CRC32;
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86 A.A.
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GRLPVDLAEEQGHRDIARYLHAATG 85
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STRAIN-C57BL/6J;
MALUMBRES M., PELLICER A.;
Submitted (JUL-1997) to the ENER; AF015460; AAB94534.1; -...
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
86
9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 AA; 9237 MW;
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91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.5%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 92.9%, les 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 91.8%;
les 78; Conservative
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PRELIMINARY;
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Gaps

111 GRLPVDLAEELGHRDVARYLRAAAG 135

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Created) PRT;

921C2 PRELIMINARY;
0921C2, 0921C2, 001-MAY-1999 (TREMBLEEL. 10, C. 01-MAY-1999 (TREMBLEEL. 10, L4 01-NOV-1999 (TREMBLEEL. 12, L4

SEQUENCE FROM N.A. STRAIN-SPRET/EI

RESOLA - 099 - 010 -

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Xiphophorus helleri.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Buteleostei; Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidei; Poeciliidae; Xiphophorus.
                                                         LITAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMMGSSEVARLLLIRGADPNVIDK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LITAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMMGSSEVARLLLTRGADPNVTDK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PANCREAS;

TOORSERSON K.D., JONES P.A.;

"Itssue-specific alternative splicing in the human INK4a/ARF cell cycle regulatory locus.";

Cycle regulatory locus.";

Cycle regulatory 1998).

EMBL; AF115544; AAD11437.1; -.

HSSP; P42771; 1B17.
                                                                                                                                     67 STGATPLHDAARTGFLDTVQLLVKAGADPQARDKDNCLPIDLARQNGHTDVVAVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 STGATPLHDAARTGFLDTVQLLVEAGADPQARDKDNCLPIDLARQNGHTDVVAVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RIO SARABIA;

KAZIANIS S., MORIZOT D.C., DELLA COLETTA L., JOHNSTON D.A.,
WOOLCOCK B., VIELKIND J.R., NAIRN R.S.;
"Comparative Structure and Characterization of a CDKNZ Gene in
XIPPhophorus FISh Melanoma Model.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF132500; AAD21313.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 124;
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Pred. No. 2.22e-51;
18; Mismatches 33; Indels
Indels
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Last annotation update)
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Last annotation update)
19; Mismatches 32;
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Pred. No. 1.89e-43;
5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AA; 12212 MW; 4F3701CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AA; 13049 MW; DA386E94 CRC32;
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                                                                                                                                                                                                                                     124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLE1. 10, Created)
01-MAY-1999 (TREMBLE1. 10, Last sequ
01-NOY-1999 (TREMBLE1. 12, Last anno'
CYCLIN-DEPENDENT KINASE INHIBITOR P12
                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                          12,
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Best Local Similarity 55.7%;
Matches 64; Conservative
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Best Local Similarity 82.0%;
Matches 50; Conservative
64; Conservative
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Q9W6I8
Q9W6I8;
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095440
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Matches
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MORIZOT D.C.;
                                                                                                                                                                                                                                                                                                                               SANTOS J.; WELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M., PELALAUNDEZ-PYQUERAS J.;
PELLICER A., FERNANDEZ-PYQUERAS J.;
"COmparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

EMBL: 079634; AAD00236.1; -.
EMBL: 079634; AAD00236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xiphophorus maculatus (Southern platyfish).
Eukaryota, Metazao; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidel; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VMMMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A CDKN2-like polymorphism in Xiphophorus LG V is associated with UV-B-induced melanoma formation in platyfish-swordtail hybrids."; Proc. Natl. Acad. Sci. U.S.A. 93:13042-13047(1996).
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                                                                                                                                                                                                                Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 480; DB 11; Length 113
Pred. No. 7.77e-74;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAZIANIS S., NAIRN R.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL: U69273; AAB09560.3; -.
HSSP; P42771; 1B17.
                                                                                                                                   01-MAY-1999 (TIEMBLIE]. 10, Last sequence update)
01-NOV-1999 (TIEMBLIE]. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 113 113 113 113 AW; 1D82E6DF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BFB0B9C5 CRC32;
                                                                             113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA
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PRT;

PRELIMINARY;

"T 9 P70067 P70067;

01-FEB-1997 (TrEMBLrel. 02, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12, CDNK2X PROTEIN.

SEQUENCE FROM N.A. STRAIN-JP 163 A; TISSUE-MUSCLE; MEDLINE; 97075115.

CONTRACTOR OF THE CONTRACTOR O

124 AA; 13034 MW;

REVISIONS

Best Local Similarity

Query Match SEQUENCE

111 GRLPVDLAEELGHRDVARYLRAAA 134

84

GRLPLDLAQERGHQDIVRYLRSAG

61

윤 ð 쉱 ò

Query Match
44.5%;
Best Local Similarity 73.8%;
Matches 62; Conservative

Kinase; Cyclin. NON_TER 1 NON_TER SEQUENCE ö

Gaps

75

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Gaps

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NON_TER
NON_TER
SEQUENCE
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                                                                                        0921C3
0921C3
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-SKIN;
RIEDER S., CHECA-CORTES M.L., JOERG H., STRANZINGER G.;
"An equine sequence homologous to cyclin-dependent kinase inhibitor (CDKNZA).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076782; AAC97110.1;
HSSP; P42771; 1B17.
Kinase; Cyclin.
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STRAIN-A/J, A/WY, AKR/J, SJL/J, SWR/J, ST/J, LP/J, LS/IBG, SM/J,
HS/IBG, BID.
HS/IBG, BID.
HSRZOG C.R., YOW M.;
Polymorphisms and chromosomal mapping of the murine pi6INK4a tumor
suppressor gene..;
Submitted (MAR-1996) to the EWBL/GenBank/DDBJ databases.
EMBL, 051567; AAD09455.1;
HSSP: Q60773; JAP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PNGVNGFGRRPIQVMMMGSVHVAELLLLHGADPNRADPDTLTRPVHDAAREGFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eguus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Perissodactyla; Eguidae; Eguus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Score 198; DB 11; Length 42; larity 71.4%; Pred. No. 2.67e-17; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P161NK4A TUMOR SUPPRESSOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 330; DB 6; 1
Pred. No. 7.63e-43;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE8139C2 CRC32;
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42 AA; 4402 MW; 3CA62FIF CRC32;
                                                                                                                                                                                                                                                                                                            58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 58
58 AA; 6162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 83.3%;
les 45; Conservative
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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hes 30; Conserv
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NON_TER
SEQUENCE
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Best Local S
Matches 4
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SEQUENCE
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0921E8
0921E8;
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097886
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STRAIN-SPRET/EI:
SANTO-SPRET/EI:
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
ENBL: U79629: AD00235.1;
ESSP: Q60773: 1AP7.
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                                                                                                                                                                                                                                                                                Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
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STRAIN-WISTAR; TISSUE-BRAIN;
COSENTINO M.T., JONES O.T.;
SUDMITTED (1905-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U65916; AAB47551.1; -.
HSSP; 000421; IANC.
PFAM; PF00023; ank; 22.
NON_TER
                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOY-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 194; DB 11;
Pred. No. 1.42e-16;
7; Mismatches 6
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P97582 PRELIMINARY;
P97582 01-MAY-1997 (TIEMBLEEL 03, C)
01-MAY-1997 (TIEMBLEEL 03, LA
01-NOV-1999 (TIEMBLEEL 12, LE
ANKYRIN (FREGMENT).
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SEQUENCE 42 AA; 4416 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.0%;
Matches 29; Conservative
                                                                                                                     PRELIMINARY;
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Search completed: Thu Jul 20 08:36:32 2000 Job time: 21 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:38:10 2000; MasPar time 6.72 Seconds 483.073 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-4
(1-137) from USO9016869A.pep
977
1 MREBNKGMPSGGGSDEGLAT.....LAEERGHRDVAGYLRTATGD 137 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:genesedp a-geneseq36

Mean 30.377; Variance 133.757; scale 0.227 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Pred. No. | 3.58e-75 | 3.58e-75 | 3.58e-75 | 3.58e-75 | 3.58e-75 | 3.58e-75 | 5.05e-74 | 1.33e-65 | 1.09e-59 | 6.31e-59 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 | 1.66e-53 |
|-------------------------------|-----------------------|------------------------|-----------------------|------------------------|-----------------------|---------------------|-----------------------|----------|-----------------------|-----------------------|-----------------------|------------------------|------------------------|------------------------|---------------------|------------------------|------------------------|------------------------|------------------------|------------------------|----------|------------------------|-----------------------|
| Description | Human multiple tumour | Multiple tumour suppre | Amino acid sequence 2 | A human multiple tumou | Human multiple tumour | Human MTS2 protein. | Cell-cycle regulatory | | Cell-cycle regulatory | Mouse multiple tumour | Human multiple tumour | A human multiple tumou | Tumour suppressor p16. | Amino acid sequence of | Human MTS1 protein. | Truncated p27/p16 fus1 | Truncated p27/p16 fus1 | Truncated p27/p16 fusi | Human p16p27 fusion pr | Human p16p27 fusion pr | ry fusic | Human p16(GS)p27 fusto | CDK inhibitory fusion |
| A | R80948 | R81702 | W74553 | W80526 | W19255 | W40526 | R85117 | R85115 | R85118 | W70823 | W19251 | W80524 | W10627 | W74549 | W40524 | W95105 | W95106 | W95103 | W95096 | W95107 | W23536 | W95095 | W23535 |
| DB | н | Н | Н | ч | Н | Н | - | ч | Н | Н | - | Н | Н | Н | -1 | Н | - | Н | - | - | н | Н | - |
| % Query Match Length DB | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 130 | 130 | 156 | 156 | 156 | 156 | 156 | 237 | 252 | 334 | 365 | 365 | 365 | 380 | 380 |
| Query Match | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 92.8 | 83.8 | 77.5 | 76.7 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 |
| Score | 919 | 919 | 919 | 919 | 919 | 919 | 907 | 819 | 757 | 749 | 692 | 692 | 692 | 692 | 692 | 692 | 692 | 692 | 692 | 692 | 692 | 692 | 692 |
| Result No. | - | 7 | m | 4 | ហ | 9 | 7 | œ | 0 | 10 | 11 | 12 | 13 | 14 | 13 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 |

| 11.488888888888888888888888888888888888 |
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| Multiple tumour suppre Human multiple tumour Inhibitor of cyclin de Cell-cycle regulatory Human p27-p16 fusion PCDK inhibitory fusion Human multiple tumour Human multiple tumour Truncated p27/p16 fusi Amino acid sequence 1 Multiple tumour Sequence 1 Multiple tumour RISEL-beta prot Human multiple tumour Human multiple tumour Human multiple tumour Cell-cycle regulatory Cell-cycle regulatory Cell-cycle regulatory Cell-cycle regulatory Cell-cycle regulatory Cell-cycle regulatory |
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ALIGNMENTS

Query Match
94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels

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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60

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Jiang P, Kamb A, S.
WPI; 99-044585/04.
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JS5843756-A.
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Matches
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Mr.PSDB; 700745.

Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening buschosure; Page 103; 148pp; English.

An individual can be diagnosed as having a predisposition to cancer hay detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS2 gene OKF 100745 (which encodes RB1702). The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.
1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMMGSAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MREENKGMPSGGGSDEGLASAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSAR 60
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04-DEC-1998 (first entry)
Amino acid sequence 2 of the multiple tumour suppressor MISIEIS.
Amintiple tumour suppressor; MISIEIS; human; cancer; hybridisation;
somatic mutation; gene therapy.
Homo sapiens.
01-SEP-1998.
07-JUN-1995; 480810.
                                         VAELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA
                                                                                                                                                                                                                                                                                           08-MAY-1996 (first entry)
Multiple tumour suppressor 2 (MTS2) polypeptide.
Multiple tumour suppressor; MTS2; cancer; diagnosis; assay; predisposition; melanoma; leukaemia; lymphoma; prognosis; prodisposition; melanoma; leukaemia; lymphoma; prognosis; Homo sapiens.
W09525813.Al.
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Pred. No. 3.58e-75;
3; Mismatches 2; Indels
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18-MAR-1994; US-214582.
18-MAR-1994; US-215087.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
(MYRI-) MYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A, Skolnick MH;
WPI: 95-344626/44.
                                                                                                                                                                                                                                           R81702 standard; Protein; 138 AA. R81702;
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W74553 standard; Protein; 138 AA.
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Local Similarity 95.7%;
les 132; Conservative
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Matches
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AC W7
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mutation(s)
Sizolosure; Fig 11; 73pp; English.

This is the amino acid sequence of the multiple tumour suppressor
This is the amino acid sequence of the invention. The MTS gene
(MTSIELS) protein, used in the method of the invention. The MTS gene
is useful in the diagnosis and prognosis of human cancer, e.g. by
standard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein mimetics, also for therapeutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human multiple tumour suppressor 2 (MTS2) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, asstrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 94.1%; Score 919; DB 1; Length 138; Local Similarity 95.7%; Pred. No. 3.58e-75; nes 132; Conservative 3; Mismatches 2; Indels
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A human multiple tumour suppressor 2 (MTS2) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer
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W80526 standard; Protein; 138 AA.
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07-JUN-1995; US-480810.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; WO-U03316.
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28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS
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Useful for the diagnosis of cancers related to MTSIEL-beta mutation (s) and their treatment mutation (s) and their treatment bisclosure; Fig il; 72pp; English.

This sequence represents a human multiple tumour suppression protein, This sequence represents a human multiple tumour suppression protein, This sequence represents a human multiple tumour suppression protein, This sequence represents a human multiple tumour suppression protein, This sequence represents a human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemla, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell-cycle regulatory protein p15.
Cell-cycle regulatory protein p15.
Cell-cycle regulatory protein p15.
Cell-cycle regulatory protein p15.
CCR; cancer; cell proliferation.
Homo sapiens.
W09528483-A1.
26-OCT-1995.
M4-APR-1995; U04636.
M4-APR-1994; US-227371.
25-MA-1994; US-248812.
M4-SEP-1994; US-346147.
CCLD-COLD SPRING HARBOR LAB.
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R85117 standard; Protein; 138 AA.
                                                                                                                                                                                   (MYRI-) MYRIAD GENETICS INC.
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01-MAR-1996 (first entry)
             14-APR-1998.
07-JUN-1995; 487033.
07-JUN-1995; US-487033.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
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MTS2; multiple tumour suppressor; diagnosis; cancer;
germ-line mutation; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                                                                                               W19255 standard; Protein; 138 AA.
W19255 standard; Protein; 138 AA.
W19255 10. SEP-1997 (first entry)
Human multiple tumour suppressor 2 gene product.
Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.1%; Score 919; DB 1; Length 138; 95.7%; Pred. No. 3.58e-75; vative 3; Mismatches 2; Indels
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production of recombinant mutant polypeptide(s)
Disclosure; Columns 73-74; 72pp; English.
The present sequence the human multiple tumour suppressor
(MTS2) gene product, useful in cancer diagnosis.
Sequence 138 AA;
                                    DB 1; Length 138;
                                                                       Indels
                                                    Pred. No. 3.58e-75;
                                                                       3; Mismatches
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                                  Score 919;
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18-MAR-1994, US-214582.
18-MAR-1994, US-215086.
18-MAR-1994, US-215087.
14-APR-1994, US-227369.
01-JUN-1994, US-227369.
01-JUN-1994, US-251938.
17-MAR-1995, US-251938.
07-JUN-1995, US-251938.
07-JUN-1995, US-251938.
07-JUN-1995, US-274177.
07-JUN-1995, US-274177.
07-JUN-1995, US-274177.
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WPI; 97-258217/23.
N-PSDB; T69781.
                                  94.1%;
95.7%;
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                                                    Local Similarity 95.7%;
nes 132; Conservative
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Matches 132; Conservative
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Sequence
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                                                                                                                                                                                                   60 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                  Cell-cycle regulatory protein p15 homologue.
Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
CCR; cell proliferation; agonist; antagonist.
                                                                                                                                                                              61 VAELLLLHGAEPNCADPATLTRPVHDAARERFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
                                                                                                                           1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSAR 59
                                                                                                        1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVWMMGSAR 60
                                                                    Gaps
                                                                      ij
                              Score 907; DB 1; Length 138;
Pred. No. 5.05e-74;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01. .102
note= "unidentified amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
57. .59
/note= "unidentified amino acids"
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. .67
note= "unidentified amino
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                                                                                                                                                                                                                                                                                                                                              n 8
885115; standard; Protein; 138 AA.
R85115;
01-MAR-1996 (first entry)
                                                                                                                                                                                                                                                       EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                                                                                           FERGHRDVAGYLRTATGD 137
                                Query Match 92.8%;
Best Local Similarity 94.9%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference 128. .130
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138 AA;
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Sequence
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p15, showing at least 60% homology to p15 (R85117), functions as either an agonist or antagonist of cell cycle regulation.
Sequence 138 AA;
                                                                                                                                                                                                                                                                                   Cell-cycle regulatory protein p15.
Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
CCR; cancer; cell proliferation.
                                                                                                                                                                                          9
                                                                                                                                                                                                                   1 MREENKGMPSGGGSDEGLAIPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVWMMGSARV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGSSDAGLATAAARGQVETVRQLLEAGADPNALNRFGRRPIQVMMMGSARVAELLLLHGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Claim 9; Page 81-82; 109pp; English.

The mouse cell-cycle regulatory (CCR) protein p15 (R85118) was obtd. by expression of a cDNA clone (T02964) isolated from mouse embryonal carcinoma cells. CCR p15 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative disorders.
                                                                                                                                                                                          1 MREENKGMPSGGGSDEGLATPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGXXXV
                                                                                             Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 130;
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Pred. No. 1.09e-59;
10; Mismatches 7; Indels
                                                                                        Score 819; DB 1; Length 138 Pred. No. 1.33e-65; 0; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hannon GJ, Serrano
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W70823 standard; Protein; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n 9
R85118 standard; Protein; 130 AA.
R85118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1994; US-227371.
25-WAY-1994; US-248B12.
14-SEP-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
                                                                                          83.8%;
larity 82.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                  XEXGHXDXXXXLRXAXGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 77.5%;
Best Local Similarity 85.9%;
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            120 EERGHRDVAGYLRTATGD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W70823;
03-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demetrick DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1995; U04636
                                                                                                                   Best Local Similarity
Matches 114; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 AA;
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WPI; 95-373798/48.
N-PSDB; T02964.
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Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoma Disclosure; F1g 1b; 92pp; English.

This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in eukaryotic cells and
                                                                                                                     76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human multiple tumour suppressor I (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 ATLITRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4; cancer cell; lung cancer; bladder cancer; melanoma; restenosis; the anti-angiogenic activity; hyperproliferative disorder.

W09703635-A2.
                                                                                                                                                 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

70.8%; Score 692; DB 1; Length 156; Best Local Similarity 85.8%; Pred. No. 1.66e-53; Matches 103; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                        W80524;
03-FEB-1999 (first entry)
A human multiple tumour suppressor 1 (MTS1) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Columns 65-66; 80pp; English.
                                                                                                                                                                                                                                                                T 12
W80524 standard; Protein; 156 AA.
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W10627 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC
JAMP, 99-044585/04.
N-PSDB: V70583.
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17-JUL-1996; U11787.
17-JUL-1995; US-502881.
(TEXA) UNIV TEXAS SYSTEM.
JIN X, ROLH J;
WPI: 97-132336/12.
N-PSDB; T60951.
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28-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
US5843756-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIAR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 GGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVAMAGSARVAELLLLHGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GGSSDAGLATAAARGQVETVRQLLEAGADPNALNRFGRRPIQVMMGSAQVAELLLLHGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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    useful for primer

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Human multiple tumour suppressor 1 gene product.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
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Pred. No. 6.31e-59;
11; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
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Mouse multiple tumour suppressor 2 (MTS2) protein.
Murine; multiple tumour suppressor 2 gene; MTS2; cancer.
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Pred. No. 1.66e-53;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                             Mouse multiple tumour suppressor gene segment
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                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Fig 19; 80pp; English.
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18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN-1994; US-221938.
17-MAR-1995; WO-U03537.
07-JUN-1995; US-2414177.
(MYRI-) WYRIAD GENETICS INC.
(UTAH) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTAH ) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A,
WPI; 97-258217/23.
                                                                                                                                              28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC.
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|larity 85.8%;
| Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.2%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                Jiang P, Kamb A, Stone S; WPI; 99-044585/04.
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nes 103; Conser
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| 130 YLRTATGD 137
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                                                                                                                  01-DEC-1998
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Best Loca Matches

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Disclosure; Column 63-64; 73pp; English.

This is the amino acid sequence of the multiple tumour suppressor 1

This is the amino acid sequence of the multiple tumour suppressor 1

(MTS-1) protein, used in the method of the invention. The MTS gene
(Strated) in the diagnosis and prognosis of human cancer, e.g. by
standard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein mimerics, also for therapeutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
sequence 156 AA;
used in the expression construct of the invention. pl6 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 settivity, and functions as a tumour suppressor. By detected whis sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore pl6 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inscrted in the antisense orientation, the expression construct inhibits also function. Reduced or increased levels of pl6, or a related nucleic acid, may be diagnostic of tumours, e.g. by southern or Northern blot, antibody immunoblot, fluorescent cell sorting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 LAIPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMMGSARVAELLLLHGAEPNCADP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of multiple tumour suppressor 1. Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                         Score 692; DB 1; Length 156;
Pred. No. 1.66e-53;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 14
W74549 standard; Protein; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MYRI-) MYRIAD GENETICS INC.
Kamb A;
WPI; 98-494842/42.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.8%;
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1998

07-UN-1995; 480810.

07-UN-1995; 08-2480810.

18-MAR-1994; US-214582.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UNR-1994; WO-U03316.
                                                                                                                                                                                                                                                                                                                  156 AA;
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                                                                                                                                                                                                                                                                                             or immunoassay
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US5801236-A.
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WTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use pecific for Multiple Tumour Suppressor IEI-beta gene - are useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment bisclosure. Column 63-64; 72pp; English.

This sequence represents a human multiple tumour suppression protein, MTSI. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, eg. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                               76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                       LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP 75
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   LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 692; DB 1; 1
Pred. No. 1.66e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                              n 15
W40524 standard; Protein; 156 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match
Local Similarity 85.8%;
hes 103; Conservative
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15-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN 1995; US-487033.

18-MAR-1994; US-21586.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; US-25138.

17-MAR-1995; WO-U03316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MTS1 protein.
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N-PSDB; V11238.
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Search completed: Thu Jul 20 08:38:18 2000 Job time: 8 secs.

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Gaps

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Score 692; DB 1; Length 156; Pred. No. 1.66e-53; 6; Mismatches 10; Indels

Query Match 70.8%; Best Local Similarity 85.8%; Matches 103; Conservative

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:40:10 2000; MasPar time 5.21 Seconds 379.758 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869a-4 (1-137) from US09016869a.pep 977 I MREBNKGWPSGGGSDEGLAT......LAEERGHRDVAGYLRTATGD 137 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

145341 segs, 14437480 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Mean 28.536; Variance 128.899; scale 0.221 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Pred. No. | 2.17e-79 | 2.17e-79 | 1.06e-77 | 92e-74 | 5.92e-74 | 5.92e-74 | 5.92e-74 | 92e-74 | 92e-74 | 5.92e-74 | .92e-74 | 92e-74 | 5.92e-74 | 5.92e-74 | 1.32e-64 | 7.98e-59 | .98e-59 | 7.98e-59 | 4.44e-58 | 82e-53 | 82e-53 | 82e-53 | 82e-53 |
|--------|--------------------------|------------|------------|------------|------------|-------------|------------|-------------|------------|------------|------------|------------|------------|-------------|------------|----------------|------------|------------|------------|-------------|------------|------------|------------|------------|
| | Prec | 2 | 7 | 7 | ŝ | S. | ď. | 5 | 'n | 'n | 'n | ς. | 'n | 'n. | Ś | - i | ~ | ~ | <u>'</u> | 4. | œ. | ω | œ | œ |
| | | Applicatio | Applicatio | Applicatio | Applicatio | , Applicati | Applicatio | , Applicati | | | | | Applicatio | , Applicati | | , Applicati | Applicatio | Applicatio | Applicatio | , Applicati | Applicatio | Applicatio | Applicatio | Applicatio |
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| | Description | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| SOMMAN | CI CI | US-08-306- | US-08-893- | PCT-US96-0 | PCT-US95-0 | US-09-120- | US-08-581- | US-08-486- | US-08-508- | US-08-480- | US-08-384- | US-08-474- | US-08-627- | US-08-848- | US-08-487- | US-08-581- | PCT-US95-0 | US-08-627- | US-08-581- | US-08-508- | US-08-480- | US-08-474- | US-08-487- | us-09-120- |
| | DB | ~ | ~ | 4 | 4 | m | m | ~ | ~ | - | m | Н | n | N | -1 | m | 4 | N | m | ~ | -1 | н | - | m |
| | Query Match Length DB | 137 | 137 | 136 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 138 | 130 | 130 | 130 | 130 | 156 | 156 | 156 | 156 |
| æ | Query Match | 100.0 | 100.0 | 98.2 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 94.1 | 83.8 | 77.5 | 77.5 | 77.5 | 76.7 | 70.8 | 70.8 | 70.8 | 70.8 |
| | Score | 977 | 977 | 959 | 919 | 919 | 919 | 919 | 919 | 919 | 919 | 919 | 919 | 919 | 919 | 819 | 757 | 757 | 757 | 749 | 692 | 692 | 692 | 692 |
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| 692 70.8 156 2 US-08-508- Sequence 2, Applicatio 8.82e-53 692 70.8 156 2 US-08-848- Sequence 2, Applicatio 8.82e-53 692 69.8 148 4 PCT-US93-0 Sequence 1, Applicatio 7.48e-52 69.8 148 3 US-08-384- Sequence 16, Applicatio 7.48e-52 69.8 148 3 US-08-384- Sequence 24, Applicatio 7.48e-52 69.8 148 1 US-08-154- Sequence 2, Applicatio 7.48e-52 69.8 156 4 PCT-US95-0 Sequence 2, Applicatio 7.48e-52 69.8 156 2 US-08-51- Sequence 2, Applicatio 7.48e-52 682 69.8 156 2 US-08-51- Sequence 2, Applicatio 7.48e-52 69.8 157 4 PC-US96-0 Sequence 2, Applicatio 7.48e-52 69.8 159 1 US-08-59- Sequence 3, Applicatio 7.52e-47 59.8 105 2 US-08-51- Sequence 3, Applicatio 7.52e-47 59.5 105 2 US-08-51- Sequence 14, Applicatio 1.11e-41 572 58.5 105 2 US-08-48- Sequence 14, Applicatio 1.11e-41 572 58.5 105 1 US-08-508- Sequence 14, Applicatio 1.11e-41 572 58.5 105 1 US-08-508- Sequence 14, Applicatio 1.11e-41 572 58.5 105 1 US-08-508- Sequence 14, Applicatio 1.11e-41 11e-41 11e-4 | ALIGNMENTS 1 08-306-511A-4 STANDARD; PRT; 137 AA. XXX | Sequence 4, Application US/08306511A Sequence 4, Application US/08306511A Patent No. 5962316 GENERAL INFORMATION: APPLICANT: Demetrick, Douglas J. APPLICANT: Genetrick, Douglas J. APPLICANT: Genetrick, Douglas J. APPLICANT: Hannon, Gregory J. TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Oses TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses TITLE OF INVENTION: CORRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STREET: 60 State Street CITY: Boston STREET: Roston STREET: Rosto |
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                                                                                           61 AELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAE 120
                                                      1 MREENKGMPSGGGSDEGLATPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMMGSARV 60
                                                              0; Gaps
                                                                                                                                                                                                                                                          Sequence 4, Application US/08893274
Patent No. 596881
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                  Length 137;
                Score 977; DB 2; Length 137;
Pred. No. 2.17e-79;
0; Mismatches 0; Indels
                                                                                                                                                                                     137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-UULY-1997
CLASSIFICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FOLEY, HOAG & BLIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
                                                                                                                                                                                       PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
137 AA; 14746 MW; 80670 CN;
                                                                                                                                                                                                                                             Sequence 4, Application US/08893274
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                       STANDARD;
                Query Match
Best Local Similarity 100.0%;
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                Length 137;
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Pred. No. 2.17e-79;
0; Mismatches 0; Indels
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ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: FILIPPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252
FILING DATE: NOT YET ASSIGNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application PC/TUS9605252
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: p19: A Cell Cycle Inhibitor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATORNEY AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 AA
                REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMUNICATION INFORMATION:
TELEPRONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                             MOLECULE TYPE: protein
JENCE 137 AA; 14746 MW; 80670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application PC/TUS9605252
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TELEFAX: (415) 543-5643
INFORMATION FOR SEC ID NO: 6: SEQUENCE CHARACTERISTICS:
NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ERGHRDVAGYLRTATGD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ERGHRDVAGYLRTATGD 137
                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US96-05252-6
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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
                                                                                                                                                                                                                                                                                                                                                                                                              138 AA.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UNN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18 WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/27,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/21,569
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/21,569
FILING DATE: 11-APR-1994
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09120130
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09120130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                  121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                                                                                                           120 EERGHRDVAGYLRTATGD 137
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
20005
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US-09-120-130-16
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                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses TITLE OF INVENTION: Related Thereto NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: PROPER COMPATIBLE OF COMPATIBLE 
                                                                                                                                                                                                                                                               Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 138;
                                                                                                                                                                                                                                                               Query Match 98.2%; Score 959; DB 4; Length 136
Best Local Similarity 99.3%; Pred. No. 1.06e-77;
Matches 136; Conservative 0; Mismatches 0; Indels
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                                                                                                                                         NAME/KEY: Protein
LOCATION: 1.136
OTHER INFORMATION: /note= "human p15"
NCE 136 AA: 14689 NW; 79498 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/306,511
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-NAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.1%; Score 919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
ENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application PC/TUS9504636
LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ERGHRDVAGYLRTATGD 136
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                      TYPE: amino
STRANDEDNESS:
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PCT-US95-04636-4
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US-08-486-047-16
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Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Beannon, Gregory J.
TILLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TILLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                             60 VAELILLHGAEPNCADPAILTRPVHDAAREGFLDILVVLHRAGARLDVRDAWGRLPVDLA 119
                                                                                                                                                   61 VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
                                                                                                            1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
                                                                                                                               1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSAR 59
                                                                                          1; Gaps
                                                                    Score 919; DB 3; Length 138; Pred. No. 5.92e-74; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                     138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Wordead
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/248,812 FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
                                                                                                                                                                                                                                                     PRT;
                                      MOLECULE TYPE: protein
FENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08581918A
                                                                                                                                                                                                                                                     STANDARD;
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                     Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                          121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                    120 EERGHRDVAGYLRTATGD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-08-581-918A-4
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                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
- ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUMTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 919; DB 3; Length 138 Pred. No. 5.92e-74; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 AA.
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: VIncent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 138 AA; 14722 MM; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 17-MAR-1995
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FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US95/0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSAR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08480810
Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
CORRESSEDNOBNCE ADDRESS:
ADDRESSED: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 919; DB 2; Length 138;
Pred. No. 5.92e-74;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEFORMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 anino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 EERGHRDVAGYLRTATGD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 919; DB 2; Length 138;
Pred. No. 5.92e-74;
3; Mismatches 2; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: 47
CORRESPONDENCE ADDRESS: ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
STATE: DC
COUNTRY: USA
ZIANE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 AA
                                                                                                                                                                                                                                                                                        24884-109348-B
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION POR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08508735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 EERGHRDVAGYLRTATGD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.1%;
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 8
US-08-508-735-16
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
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Patent No. 5624819
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GENALINE MUTATIONS IN THE MTS GENE
NUMBER OF SECONESES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.050000
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
         ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AA.
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Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
JENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08474177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
                                                      Washington
                                                      CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jr 11
US-08-474-177-16
                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
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Pred. No. 5.92e-74;
3; Mismatches 2; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202-962-4810
TELEFAX: 202-962-8300
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/08384106A
Patent No. 6033847
GENERAL INFORMATION:
APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Downing M.D., James
APPLICANT: Hiral Ph.D., Hiroshi
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/08384106A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EERGHRDVAGYLRTATGD 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-384-106A-25
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Sequence 16, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
SPELICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon Albright, Lisa A.
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
              TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle TITLE OF INVENTION: Regulation NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.1%; Score 919; DB 2; Length 138; Best Local Similarity 95.7%; Pred. No. 5.92e-74; Matches 132; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 AA
                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
ATTONNEY, FAGENI INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE, POCKET NUMBER: CSI-001CP6
TELECOMUNICATION INFORMATION:
TELECHNE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08848251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 EERGHRDVAGYLRTATGD 138
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                                                                                                             STREET: 60 Sta
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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US-08-848-251-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.1%; Score 919; DB 1; Length 138; Best Local Similarity 95,7%; Pred. No. 5.92e-74; Matches 132; Conservative 3; Mismatches 2; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: US 08/215,086
FILING DATE: US US WAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: US US WAR-1994
PRIOR APPLICATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 22,996
INFORMATION FOR SED ID NO: 16:
SEROBENE CHRARATERISTICS:
LPWATH: 13A RMIND ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08627610
Patent No. 5919997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Depinho, Ronald A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08627610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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US-08-627-610-4
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Sequence 16, Application US/08487033 Patent No. 5739027 GENERAL INFORMATION:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 EERGHRDVAGYLRTATGD 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VAELLILHGAEPNCADPATLITRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVWMGSAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.1%; Score 919; DB 2; Length 138; Best Local Similarity 95.7%; Pred. No. 5.92e-74; Matches 132; Conservative 3; Mismatches 2; Indels
                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AA.
                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTONNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24,884-10934
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
INFORMATION FOR SEQ 1D NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
ENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08487033
                                                                                                                                                                                                                                                                                                                                                                                                                                         : 138 amino acids
amino acid
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                                       COMPUTER READABLE FORM:
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CITY: Washington
           USA
20005
                                                                                                                FILING DATE
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                    COUNTRY:
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Pred. No. 5.92e-74;
3; Mismatches 2; Indels 1; Gaps
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APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSIEI-Beta GENE
NUMBER OF SEQUENCES: 36
NUMBER OF SEQUENCES: 36
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ENCE 138 AA; 14722 MW; 80871 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Search completed: Thu Jul 20 08:40:18 2000 Job time : 8 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:38:35 2000; MasPar time 10.90 Seconds 592.803 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-4
(1-137) from USO9016869A.pep
977
1 MREBNKGMPSGGGSDEGLAT.....LAEERGHRDVAGYLRTATGD 137 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

142080 segs, 47172406 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir63 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 42.515; Variance 86.121; scale 0.494

SUMMARIES

| | | d | | | | | |
|---------------|-------|----------------|--------|----|----------|-----------------------|-----------|
| Result No. | Score | Query Match | Length | 80 | A | Description | Pred. No. |
| 1 | 919 | 94.1 | 138 | ~ | B55479 | CDK4 inhibitor p14(IN | 7.51e-158 |
| 7 | 749 | 76.7 | 130 | N | 178845 | p15INK4b - mouse | 3.56e-123 |
| m | 692 | 70.8 | 156 | ~ | JE0141 | cyclin dependent kina | 1.22e-111 |
| 4 | 581 | 59.5 | 167 | ~ | 158352 | p161NK4a - mouse | 2.36e-89 |
| 2 | 329 | 33.7 | 164 | 7 | A57378 | cyclin-dependent kina | 3.08e-40 |
| ø | 315 | 32.2 | 166 | 7 | A57379 | CDK4/CDK6 1nh1b1tor p | 1.30e-37 |
| 7 | 312 | 31.9 | 166 | ~ | B57378 | cyclin-dependent kina | 4.74e-37 |
| 80 | 284 | 29.1 | 41 | ~ | 152720 | qene p15INK4B protein | 7.40e-32 |
| σ | 249 | 25.5 | 168 | ~ | A55479 | CDK6 inhibitor p18 - | 1.74e-25 |
| 10 | 247 | 25.3 | 168 | 7 | B57379 | CDK4/CDK6 inhibitor p | 3.99e-25 |
| 11 | 140 | 14.3 | 1423 | Н | 137275 | death-associated prot | 4.79e-07 |
| 12 | 140 | 14.3 | 1856 | ~ | B35049 | ankyrin 1, erythrocyt | 4.79e-07 |
| 13 | 140 | 14.3 | 1880 | ~ | A35049 | ankyrin 1, erythrocyt | 4.79e-07 |
| 14 | 140 | 14.3 | 1881 | - | SJHUK . | 1, | 4.79e-07 |
| 15 | 137 | 14.0 | 1848 | N | S37771 | ankyrin, erythrocyte | 1.38e-06 |
| 16 | 137 | 14.0 | 1862 | a | I49502 | ankyrin - mouse | 1.38e-06 |
| 17 | 133 | 13.6 | 2524 | ~ | A35844 | Xotch protein - Afric | 5.56e-06 |
| 18 | 132 | • | 4377 | ~ | A55575 | ankyrin 3, long splic | 7.86e-06 |
| 19 | 131 | 13.4 | 3924 | ~ | . S37431 | 7 | 1.11e-05 |
| 20 | 130 | 13.3 | 2531 | ~ | S18188 | notch protein homolog | 1.56e-05 |
| 21 | 129 | 13.2 | 1411 | ~ | S30355 | alpha-latroinsectotox | 2.20e-05 |
| 22 | 129 | 13.2 | 2318 | N | S45306 | notch 3 protein - mou | 2.20e-05 |
| 23 | 129 | 13.2 | 2555 | 7 | A40043 | ď | 2.20e-05 |

| 3.10e-03 4.36e-05 8.58e-05 1.68e-05 | .35e- .27e- .82e- | .35e- | 3.25e-03 3.25e-03 3.25e-03 3.25e-03 8.49e-03 | 1.17e-02 2.19e-02 2.19e-02 4.09e-02 1.03e-01 | |
|--|---|--|---|--|------------|
| notch3 protein - huma Notch-1 protein - mou | cell-fate determining SKD3 - mouse hypothetical protein ankyrin-like repeat p | notch protein - fruit transcription factor notch4 - mouse ankyrin-related prote | ankyrin-related unc-4 elegans ankyrin-relat ankyrin-related unc-4 ankyrin-related unc-4 G9a protein - human | probable ankyrin - sy probable fur-like tra B-cell CLL/Jymphoma 3 ankyrin - fruit fly (transcription factor | |
| S78549 A46019 A56695 | A49128 149045 T15888 B47169 | A24420 A53950 T09059 A57282 | T15345 T15346 T15344 T15347 S30385 | H71274 S77600 A34794 T13940 A35697 | ALIGNMENTS |
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| 2321 2531 638 | 2471 677 209 323 | 2703 414 1964 1786 | 1809 1815 1867 1001 | 934 1546 1549 971 | |
| 12.8 | 12.5 12.5 12.5 1.2.5 | 111.8 | 111111 7.7.7.4 | 111.1 | |
| 127 | 123 | 1111 1118 1158 | 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 110 108 106 106 | - |
| 2022 | 370 330 310 | 8 8 8 8 8 8 8 4 8 8 | 8 8 8 8 4 7 8 8 9 0 | 44444 16646 | F.111.2 |
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| 3# CDD 38 | 28-May-1999 B55479; S47593; I81183; I52713 A55479 Guan, K.L.; Jenkins, C.W.; Li, Y O'Keefe, C.L.; Matera, A.G.; X Genes Dev. (1994) 8:2939-2952 Growth suppression by p18, a p16 (INKALYMES)-related CDK6 inhi wild-type pRb function. references MUID:95095079 Ion B55479 Illeule_type mRNA sidues I-138 ##label GUA | ##cxpcsreferences GB:U17075; NID:g639715; PID:g639716 ##experimental_source HeLa cells SA7593 #authors Hannon, G.J.; Beach, D. #Journal Nature (1994) 371:257-261 #fitle D15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest. #cross-references MUID:94359613 #accession S47593 ##molecule_type mRNA ##residues 1-19, TP', 22, 24-31, 'HSW', 35-138 ##label HAN ##residues GB:L36844; NID:9556197; PIDN:AAA50282.1; PID:g556198 ##cross-references GB:L36844; NID:g556197; PIDN:AAA50282.1; PID:g556198 | ERENCE Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Hauthors Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, R.; Tavitgian, S.V.; Stockert, E.; Day III, R.S.; Johnson, B.E.; Skolnick, M.H. Schence (1994) 264:436-440 H.H. Schence (1994) 264:436-440 H.H. Schence MUID: 94204645 Harshmany tumor types. Harstally involved in genesis of many tumor types. Harstally involved in genesis of many tumor types. Harstally involved in genesis of many tumor types. Harstally involved in genesis of Harstally III.83 Hanslation not shown; translated from GB/EMBL/DDBJ ##molecule_type DNA ##molecule |
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| RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE | ACCESSIONS REFERENCE #authors #journal #title #cross-ref #accession ##nolec | ##Cross ##exper REFERENCE #dournal #fille #accession ##molec ##resid ##resid ##resid | REFERENCE #authors #journal #title #cross-ref #accession ##statu ##statu ##molec ##resid ##cross |

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Cloning and characterization of murine p16INK4a and p15INK4b
#authors Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.;
Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler,
K.W.; Vogelstein, B.
#journal Cancer Res. (1994) 54:6353-6358
#title Deletion of p16 and p15 genes in brain tumors.
#accession 152713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A. Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr, C.J.; Serrano, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
28-Feb-1997
I78845
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#length 138 #molecular-weight 14722 #checksum 1236
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#length 130 - #molecular-weight 13788 #checksum 7879
                                                                                                                                                                                                                                        #gene GDB:CDKN2B; MTS2
##scross-references GDB:579577; OMIM:600431
#map_position 9p21-9p21
KEYWORDS cell cycle control; protein kinase inhibitor; tumor
                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
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##residues 1-130 ##label RES
##cross-references GB:S79252; NID:g1087092; PID:g1087093
                                                                                                                                                                                                                                                                                                                                                                            Score 919; DB 2; Length 138
Pred. No. 7.51e-158;
3; Mismatches 2; Indels
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Local Similarity 85.2%; Pred. No. 3.56e-123;
nes 109; Conservative 11; Mismatches 7; Indels
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##cross-references GB:S75756; NID:g861470
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p15INK4b - mouse
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#accession I78845
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llarity 95.7%;
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##residues 1-52
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#fitle A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.
#cross-references MUID:94081956
#accession S39359
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Harehman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.;
Johnson, B.E.; Skolnick, M.H.
Science (1994) 264:436-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues
1-156 ##label HUA
##experimental_source Helia cell
REFERBNCE
#authors Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.;
Hussain, S.P.; Bennett, W.P.; Forrester, K.; Gerwin, B.;
Serrano, M.; Beach, D.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:11045-11049
#title Mutations and altered expression of pi6INK4 in human cancer.
#cross_references_MUID:95062202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
##residues 1-156 ##label HU2
FT This protein suppresses the function of cyclin DI/CDK4 and cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huang, C.; Deng, W.; Fu, J.
Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of P16 ink4 cDNA from hela
                                                                                                                                                                                                                                                                                                                                                            Huang, C.G.; Deng, W.; Fu, J.L.
Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of P16ink4 cDNA from hela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status preliminary
##molecule_type mRNs
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this sequence has been corrected in reference 159268
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                                                                                                                       JE0141 #type complete
cyclin dependent kinase - human
CDK4 inhibitor P16(INKA/MTS1); cyclin-dependent kinase
inhibitor 2A; multiple tumor suppressor 1 (MTS1)
#formal_name Homo sapiens #common_name man
02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change
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#cross-references MUID:94204645
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##cross-references GDB:335362; GDB:CDKN2A; OMIM:600160
#map_position 9p21-9p21
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Nature (1993) 366:704-707
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##residues 51-152 ##label RE2
##cross-references GB:S69804; NID:9546272
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#journal Mol. Cell. Biol. (1995) 15:2682-2688
#ittle Identification of human and mouse pl9, a novel CDK4 and CDK6
#cross-references MUID:95257949
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Cloning and characterization of murine p16INK4a and p15INK4b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                       16 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
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#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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cyclin-dependent kinase inhibitor p19 - human
#formal_name Homo sapiens #common_name man
08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
                                          #length 156 #molecular-weight 16532 #checksum 6490
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 #superfamily unassigned ankyrin repeat proteins
cell cycle control; protein kinase inhibitor; tumor
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                                                                     Score 692; DB 2; Length 156
Pred. No. 1.22e-111;
6; Mismatches 10; Indels
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Pred. No. 2.36e-89;
20; Mismatches 22;
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                                                                     Query Match 70.8%;
Best Local Similarity 85.8%;
Matches 103; Conservative
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Best Local Similarity 65.6%;
Matches 80; Conservative
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Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. Mol. Cell. Biol. (1995) 15:2582-2688
Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to pl6(ink4).
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##residues 1-166 ##label HIR
##cross-references GB:019597; NID:9790568; PIDN:AAC52194.1; PID:9790569
##cross-references GB:019597; NID:9790568; PIDN:AAC52194.1; PID:9790569
IFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
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#title Novel INK4 proteins, pl9 and pl8, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.
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                                                                                               #superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology #length 164 #molecular-weight 17362 #checksum 5271
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                                                                                                                                                                                                                                                                                                                                          A57379 #type complete CDE4/CDS6 inhibitor pl9 - mouse #formal_name Mus musculus #common_name house mouse 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
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Pred. No. 3.08e-40;
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Best Local Similarity 48.2%; Pred. No. 1.30e-37;
Matches 55; Conservative 19; Mismatches 38
1-164 ##label
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Best Local Similarity 46.6%;
Matches 55; Conservative
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CDK6 inhibitor p18 - human
cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
kinase CDK6 inhibitor p18
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L. Cancer Res. (1995) 55:1607-1612
Association of rat p15:NK4B/p161NK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal
                                                                         #FIGURES 10.00 1.166 ##label CHA 1.166 ##label C
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O'Keefe, C.L.; Matera, A.G.; Xiong, Y.
fjournal Genes Dev. (1994) 8:2939-2952
#title Growth suppression by pl8, a p16(INK4/MTS1)- and p14
(INK4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRb function.
#cross-references MUID:95095079
                                                                                                                                                                                                                                                                                                                                                                                     14 GARPRGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNVQDAS 73
                                                                                                                                                                                                                                                                                                                                                                                                                   gene pl5INK4B protein - rat (fragment)
#formal_name Rattus sp. #common_name rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
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Pred. No. 4.74e-37;
20; Mismatches 38; Indels
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Pred. No. 7.40e-32;
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#length 41 #checksum 3296
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                     **status preliminary
##molecule_type mRNA
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Best Local Similarity 97.6%;
Matches 40; Conservative
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Best Local Similarity 47.4%;
Matches 54; Conservative
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##molecule_type mRNA
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#journal Mol. Cell. Biol. (1995) 15:2672-2681
#title Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.
#cross-references MUD:95257948
#accession B57379
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##residues 1-168 ##label HIR
##cross-references GB:U19596; NID:9790566; PIDN:AAG52193.1; PID:9790567
##cross-references GB:U19596; NID:9790566; PIDN:AAG52193.1; PID:9790567
IFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
Cell cycle control #length 168 #molecular-weight 18066 #checksum 8831
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##residues 1-168 ##label GUA
##cross-references GB:U17074; NID:g639713; PIDN:AAC50074.1; PID:g639714
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#map_position 1p32-1p32
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin repeat proteins; ankyrin repeat cela cycle control; protein kinase inhibitor; tumor
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death-associated protein kinase (EC 2.7.1.-) - human
calmodulin-dependent protein kinase homolog; DAP kinase
#formal_name Homo saptens #common_name man
16-Feb-1996_#sequence_revision 16-Feb-1996 #text_change
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                                                                                                                                                                                                                                                       suppressor
#length 168  #molecular-weight 18127  #checksum 9379
                                                                                                                                                                                                                                                                                                                                      Length 168;
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Pred. No. 1.74e-25;
28; Mismatches 43; Indels
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Local Similarity 39.0%;
les 46; Conservative
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Local Similarity 38.2%;
nes 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis
activity is calmodulin dependent
#superfamily death-associated protein kinase; ankyrin repeat
homology; protein kinase homology
apoptosis; ATP; calmodulin binding; phosphotransferase;
serine/threonine-specific protein kinase; tandem repeat
                   A55614
Deiss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#region calmodulin binding #status predicted\
#domain ankyrin repeat homology #label ANI\
#active_site Lys\ Glu\ ASP\ Lys #status predicted
#length 1423 #molecular-weight 159161 #checksum 6280
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Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title CDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
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ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2, erythrocyte
#formal_name Homo saplens #common_name man
17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change
10-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                         catalyzes the formation of peptidyl-serine-phosphate peptidyl-threonine-phosphate using ATP
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the gamm
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                                                                                                                                                                                                                          ##residues 1-1423 ##label RES
##cross-references EMBL:X76104; NID:9434846; PID:9434847
                                                                               #fitle Genes Dev. (1995) 9:15-30
#title Identification of a novel serine/threonine
15-kD protein as potential mediators of t
interferon-induced cell death.
#cross-references MUID:95129831
                                                                                                                                                                                                                                                                *gene GDB:DAPK1; DAPK #Cross-references GDB:555932; OMIM:600831 #npp_position 9q34.1-9q34.1
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  137275; S39269
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##residues 1-18
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*product ankyrin 1, erythrocyte form 3 *status predicted
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                                                                                                                                                       #label MAT\
#product ankyrin 2.2, erythrocyte #status predicted
#label MA2\
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Pred. No. 4.79e-07;
25; Mismatches 55; Indels 8; Gaps
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ankyrin 1, erythrocyte splice form 2 - human
ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2, erythrocyte
ankyrin 2.2, erythrocyte
$formal_name Homo sapiens #common_name man
77-uul-1990 #sequence_revision 01-0ct-1992 #text_change
04-sep-1998
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domain ankyrin repeat homology #label AN23
#tcross-references GDB:118737; OMIM:182900 #map_position Bpli.2-8pli.1
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology KEYWORDS alternative splicing
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##cross-references GB:M28880
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#length 1856 #molecu
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##molecule_type mRNA
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Best Local Similarity 32.3%;
Matches 42; Conservative
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#journal Nature (1990) 344:36-42
#title Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.
#accession $808.75
##molecule_type mRNA
##residues
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#product ankyrin 2.2, erythrocyte #status predicted
#label MA2\
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#molecular-weight 206066 #checksum 6968
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AN06\
               suruk #type complete
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ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2,
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S08275; A33219; PC2220; A35443
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119 AEERGHRDVA 128
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Hermann, J.; Barel, M.; Frade, R.
Blochem. Blophys. Res. Commun. (1994) 204:453-460
Human erythrocyte ankyrin, a cytoskeleton component,
generates the p57 membrane proteinase which cleaves C3, the
third component of complement.
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#label NAT1\
#product ankyrin 2.2, erythrocyte #status predicted
#label MAT2.
##molecule_type protein

##residues 2-7, X', 9-17, X', 19-20, T', 22-30;733-749, 'A',751-753;

#28-833, XY, 835-855, XY, 857-859, XXY, 862-871;959-1003;

1106-1120, XXX, 1123-1128;1149-1172;1282-1285, E',

1287-1288;1307-1332;1345-1365, XY, 1367;1383-1427;

1601-1630;1686-1698, 'D',1700;1763-1772 ##label LUX

##note 845-Arg and 1392-Thr were also found
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#accession A35443

##molecule_type protein

##residues 'X',5,'X',7-12;403-417,'X',419-422,'H',424,'LQ';797-800,

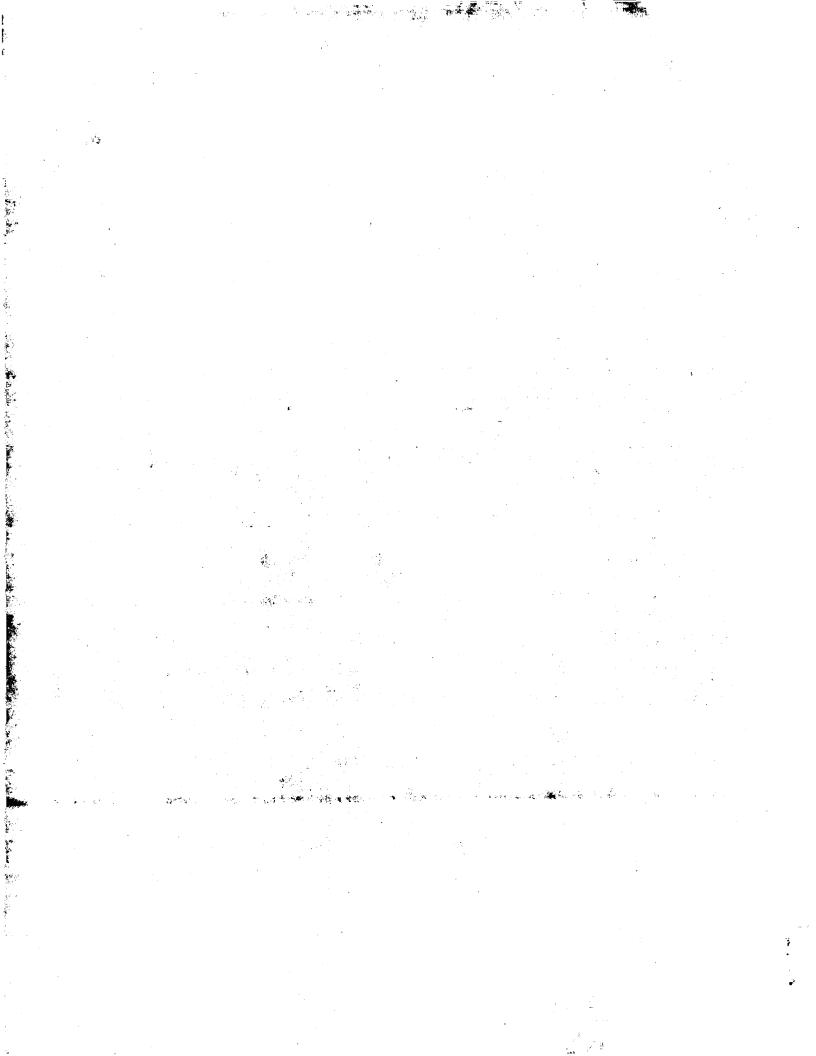
'L',802-814;862-863,'X',865-877;'X',899-901,'T',

903-909,'X',911-912 ##label DAV
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#domain ankyrin repeat homology #label AN21,
#domain ankyrin repeat homology #label AN23,
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Pred. No. 4.79e-07;
25; Mismatches 55; Indels
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##cross-references GDB:118737; OMIM:182900
##ap_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin, ankyrin repeat homology
KEYWORDS alternative splicing; phosphoprotein
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##residues 910-929 ##label HER
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#accession PC2220
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Best Local Similarity 32.3%;
Matches 42; Conservative
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Birkenmeler, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.;
Lux, S.E.; Barker, J.E.
J. Biol. Chem. (1993) 268:9533-9540
Complex patterns of sequence variation and multiple 5' and 3'
ends are found among transcripts of the erythroid ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    511 LHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG 570
                                                                                            193 NANPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRV 551
                                                                       552 AELLLERDAHPNAAGKNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHI 608
                     3 EENKGMPSGGGSDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFGRRAIQVAAM-GSARV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.0%; Score 137; DB 2; Length 1848;
Best Local Similarity 33.9%; Pred. No. 1.38e-06;
Matches 39; Conservative 21; Mismatches 48; Indels 7; Gaps
                                                                                                                                                                                                                                       S37771 #type complete
ankyrin, erythrocyte - mouse
#formal_name Mus musculus #common_name house mouse
27-May-1994 #sequence_revision 03-Aug-1995 #text_change
13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ankyrin repeat homology #label AN23
#molecular-weight 202576 #checksum 2542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status preliminary
##molecule_type mRNA
##residues 1-1848 ##label BIR
##cross-references EMBL:K69063; NID:g311816; PIDN:CAA48801.1;
PID:g311817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology #label ANI5/
homology #label AN16/
homology #label AN17/
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#accession S37771
                                                                                                                                              609 AAKQNQVEVA 618
                                                                                                                                                                                   119 AEERGHRDVA 128
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KEYWORDS
FEATURE
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Qy 76 PATLTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAM-GRLPVDLAEERGHRDVA 128

Search completed: Thu Jul 20 08:38:48 2000 Job time: 13 secs.



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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp Run on:

Thu Jul 20 08:39:06 2000; MasPar time 6.93 Seconds 602.124 Million cell updates/sec Tabular output not generated.

>US-09-016-869A-4
(1-137) from USO9016869A.pep
977
1 MREENKGMPSGGGSDEGLAT.....LAEERGHRDVAGYLRTATGD 137

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 segs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 43.541; Variance 77.735; scale 0.560 swiss-prot38 1:swissprot Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | æ | | | | | | |
|---------------|-------|----------------|--------------------------|----|------------|------------------------|------------|--|
| Result No. | Score | Ouery Match | Query Match Length DB | BB | ID | Description | Pred. No. | |
| - | 919 | 94.1 | 138 | ч | CDN5_HUMAN | CYCLIN-DEPENDENT KINAS | 7.32e-179 | |
| 7 | 751 | 76.9 | 130 | Н | CDN5_RAT | CYCLIN-DEPENDENT KINAS | 4.85e-140 | |
| m | 749 | 76.7 | 130 | Н | CDN5_MOUSE | CYCLIN-DEPENDENT KINAS | Н | |
| 4 | 692 | 70.8 | 156 | ч | CDN2_HUMAN | CYCLIN-DEPENDENT KINAS | 1.62e-126 | |
| 'n | 581 | 59.5 | 167 | Н | CDN2 MOUSE | CYCLIN-DEPENDENT KINAS | 2.75e-101 | |
| ø | 572 | 58.5 | 171 | - | CDN2_MONDO | CYCLIN-DEPENDENT KINAS | 2.96e-99 | |
| 7 | 329 | 33.7 | 166 | ч | CDN7 HUMAN | CYCLIN-DEPENDENT KINAS | 9.77e-46 | |
| œ | 315 | 32.2 | 166 | - | CDN7_MOUSE | CYCLIN-DEPENDENT KINAS | 9.05e-43 | |
| σ | 249 | 25.5 | 168 | Н | CDN6_HUMAN | CYCLIN-DEPENDENT KINAS | 4.38e-29 | |
| 10 | 247 | 25.3 | 168 | Н | CDN6_MOUSE | CYCLIN-DEPENDENT KINAS | 1.11e-28 | |
| 11 | 140 | 14.3 | 1431 | Н | DAPK_HUMAN | DEATH-ASSOCIATED PROTE | 2.39e-08 | |
| 12 | 140 | 14.3 | 1880 | ч | ANK1_HUMAN | ANKYRIN R (ANKYRINS 2 | 2.39e-08 | |
| 13 | 137 | 14.0 | 1862 | - | ANK1_MOUSE | ANKYRIN. | 7.81e-08 | |
| 14 | 133 | 13.6 | 2524 | Н | NOTC_XENLA | NEUROGENIC LOCUS NOTCH | 1 3.72e-07 | |
| 15 | 131 | 13.4 | 1839 | - | ANKC HUMAN | ANKYRIN, BRAIN VARIANT | œ | |
| 16 | 131 | 13.4 | 3924 | Н | ANKB_HUMAN | ANKYRIN, BRAIN VARIANT | 8.05e-07 | |
| 17 | 130 | 13.3 | 2531 | - | NTC1_RAT | NEUROGENIC LOCUS NOTCH | 1.18e-06 | |
| 18 | 129 | 13.2 | 2318 | Н | NTC3 MOUSE | NEUROGENIC LOCUS NOTCH | 1.73e-06 | |
| 19 | 129 | 13.2 | 2444 | ч | NTC1_HUMAN | NEUROGENIC LOCUS NOTCH | 1.73e-06 | |
| 20 | 128 | 13.1 | 2437 | - | NOTC BRARE | LOCUS | 1 2.54e-06 | |
| 21 | 125 | 12.8 | 2531 | ٦ | NTC1_MOUSE | NEUROGENIC LOCUS NOTCH | 7.91e-06 | |
| 22 | 122 | 12.5 | 677 | Н | SKD3_MOUSE | SKD3 PROTEIN. | 2.43e-05 | |
| 23 | 121 | 12.4 | 2703 | Н | NOTC_DROME | NEUROGENIC LOCUS NOTCH | 3.53e-05 | |
| | | | | | | | | |

| 1.07e-04 | 3.18e-04 | 3.82e-03 | 3.82e-03 | 2.13e-02 | 2.13e-02 | 2.99e-02 | 5.85e-02 | 5.85e-02 | 8.15e-02 | 1.13e-01 | 1.13e-01 | 1.13e-01 | 1.13e-01 | 1.13e-01 | 1.57e-01 | 1.57e-01 | 1.57e-01 | 1.57e-01 | 1.57e-01 | 1.57e-01 | 2.17e-01 |
|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|---------------|------------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|
| ANKYRIN HOMOLOG PRECUR | NEUROGENIC LOCUS NOTCH | TRANSCRIPTIONAL ACTIVA | B-CELL LYMPHOMA 3-ENCO | 2-5A-DEPENDENT RIBONUC | NUCLEAR FACTOR NF-KAPP | HYPOTHETICAL PROTEIN K | PHLB PROTEIN PRECURSOR | HYPOTHETICAL PROTEIN I | GLP-1 PROTEIN PRECURSO | SRPB PROTEIN. | GA BINDING PROTEIN BET | DEVELOPMENTAL PROTEIN | PUTATIVE GLUTAMINASE D | PHENYLALANYL-TRNA SYNT | GA BINDING PROTEIN BET | T-COMPLEX PROTEIN 1, A | HYPOTHETICAL 112.1 KD | ALPHA-LATROTOXIN PRECU |
| ANXH_CHRVI | NTC4_MOUSE | FNRL_RHOSH | BCL3_HUMAN | RN5A_MOUSE | KBF1_MOUSE | Y050_HUMAN | PHLB_SERLI | YGL1_STRCO | GLP1_CAEEL | SRPB_SYNP7 | GABD_MOUSE | CACT_DROME | GLS1_CAEEL | SYFB_THETH | GABC_HUMAN | GABC_MOUSE | GABB_MOUSE | GABB_HUMAN | TCPA_SCHMA | YKR1_CAEEL | LATA_LATMA |
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| 323 | 1964 | 248 | 446 | 619 | 971 | 740 | 227 | 341 | 1295 | 182 | 414 | 200 | 571 | 785 | 347 | 347 | 382 | 383 | 545 | 957 | 1401 |
| 12.1 | 11.8 | 11.1 | 11.1 | 10.5 | 10.5 | 10.4 | 10.2 | 10.2 | 10.1 | 10.0 | 10.0 | 10.0 | 10.0 | 10.0 | o. | 6.6 | 6.6 | 6.6 | 6.0 | 6.6 | φ. α. |
| 118 | 115 | 108 | 108 | 103 | 103 | 102 | 100 | 100 | 66 | 86 | 86 | 86 | 86 | 86 | 97 | 97 | 97 | 97 | 97 | 97 | 96 |
| 24 | 22 | 56 | 27 | 28 | 53 | 30 | 31 | 35 | 33 | 34 | 32 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| | | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

| RESULT ID C AC P DT 0 DT 0 | 1 DNS_HUMAN STANDARD; PRT; 1 42772; 1-NOV-1995 (Rel. 32, Last sequence up 1-NOV-1996 (Rel. 34, Last annotation |
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| O C C C | 2 L ^ |
| 8888 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] Spongwore FROM N a |
| 2 2 2 2 | MEDLINE: 95095079. Guan KL., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Reefe C.L., Matera G.A., Xiong Y.; |
| r r r r | "Growth suppression by pl8, a pi6INK4/MTS1- and p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; Genes Dev. 8:2939-2952(1994). |
| r r r r | <pre>SEQUENCE FROM N.A. MEDLINE; 94359613. Hannon G.J., Beach D.; "pl5INK4B is a potential effector of IGF-beta-induced cell cycle arrest.";</pre> |
| 8 | Nature 371:257-261(1994). [3] SEQUENCE OF 53-138 FROM N.A. MEDLINE; 94204645. Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K., Tavtajan S.V., Stockert E., Day R.S. III, Johnson B.E., |
| | "A cell of the regulator potentially involved in genesis of many tumor types."; Science 264:436-440(1994). [4] VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50. |
| 2444253 26677777 | MEDILINE; 93.08019.0. Okanoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Okanoto A., Hussain S.P., Hamon G.J., Shiseki M., Zariwala M., Ziong Y., Beach D.H., Yokota J., Harris C.C.; Mutations in the piclink4/mrs1/CDKN2, pisink4B/Mrs2, and pi8 genes in primary and metastatic lung cancer."; Cancer Res. 55:1448-1452[(1955)i- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST. |

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55:1607-1612(1995)
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SEQUENCE FROM N.A.
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        ij
SUBUNIT: HETERODIMER OF P14 WITH CDK4.
DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 VAEILILHGAEPNCADPATITRPVHDAAREGFIDTLVVLHRAGARLDVRDAWGRLPVDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MREENKGMPSGGGSDEGLAIPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVWMGSAR 60
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.; *Association of rat pl5INK4B/pl6INK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y., Tsuchiya H., Kikuchi Y., Mitani H.;
"Molecular genetic basis of renal carcinogenesis in the Eker rat
                                                                                                                                                                                                        Repeat; ANK repeat; Disease mutation. 2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
                                                                                                                                                                                                                                                         G -> E (IN LUNG ADENOCARCINOMA).
/FTIG=VAR_001489.
A -> V (IN LUNG ADENOCARCINOMA).
/FTIG-VAR_001489.
SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
OLL -> HSW (IN REF. 2).
WHY ODSFFEDPASFEAD21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
CADRAD2 OR INK4.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                Score 919; DB 1; Length 138;
Pred. No. 7.32e-179;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AA
                                              SIMILARITY: CONTAINS 2 ANK REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     model of tuberous sclerosis (Tsc2).";
Mol. Carcinog. 14:23-27(1995).
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23 M
34 O
14722 MW;
                                                                                                                                                               EMBL; U17075; AAC50075.1; -. EMBL; L36644; AAA50282.1; -. EMBL; S69805; AAD14049.1; -. MIM; 600411; -. Cell cycle; Anti-oncogene; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 46-86 FROM N.A. MEDLINE; 95228036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EERGHRDVAGYLRTATGD 137
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Best Local Similarity 95.7%;
Matches 132; Conservative
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138 AA;
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P55272;
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                                                        SIMILARITY).
--- SUBDUNT: HETERODIMER OF PL4 WITH CDK4.
--- SUBDUNT: HETERODICES: A SHORTER FORM MAY ARISE BY ALTERNATIVE
--- INITIATION CODONS IN THE SAME READING FRAME.
--- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
TESTIS, BARELY DEFECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
--- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
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Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
"Cloning and characterization of murine pl6INK4a and pl5INK4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CHAIN 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAG 129
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UCL-1998 (Rel. 36, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 751; DB 1; Length 130;
Pred. No. 4.85e-140;
11; Mismatches 7; Indels
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FOR THE SHORT FORM.
2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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85.2%;
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95
13748 1
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Best Local Similarity 85.2%;
Matches 109; Conservative
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PFAM; PF00023; ank;
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95380169.
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|130 YLRTATGD 137
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MEDLINE: 94338359.

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Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;

"Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41

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"Structural basis for inhibition of the cyclin-dependent kinase Cdk6
by the tumour suppressor pl6INK4a.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamoto'A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.; "Mutations in the pi6inx4/mrsi/cokn2, pl5inx4B/mrs2, and pl8 genes primary and metastatic lung cancer.";
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"The MTS1 gene is frequently mutated in primary human esophageal
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Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
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                                                  Liu Q., Harshman
SEQUENCE OF 51-152 FROM N.A.
MEDLINE; 94204645.
Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshmar
Tartigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
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                                                                                                                                                                                                                                                                                                         immortalization and senescence."; Mol. Cell. Biol. 16:859-867(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVIEW ON MELANOMA VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 9:3737-3741(1994).
                                                                                                                                                                  Science 264:436-440(1994).
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                                                                                                                                                                                                             SEQUENCE OF 1-20 FROM N.A.
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MEDLINE; 95188190.
                                                                                                Skolnick M.H.;
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                                                                                                                                                                                                                                                             Hara E.
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                                                                                                                                                                                                                                                         -i- SUBUNIT: HÉTERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-i- TISSUE SPECTIFICITY: EXPRESSED UBIQUITOUSLY.
-i- INDUCTION: BY TGF-BETA.
-i- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                         Malunbres M., de Castro I., Santos J., Melendez B., Mangues R., Serrano M., Pellicer A., Fernandez-Piqueras J.;
Serrano M., Pellicer A., Fernandez-Piqueras J.;
Inactivation of the cyclin-dependent Kinase inhibitor pi5INK4b by deletion and de novo methylation with independence of pi6INK4a alterations in murine primary T-cell lymphomas.";
Oncogene 14:131-137(0(1997).
- I. FUNCTION: INTERACTS STRONGLY WITH CDM4 AND CDM6. POTENT INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 EPNCADPALLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAG 129
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P42771; 015191;
P42771; 015191;
D42771; 015191;
D42771; 015198; Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4A)
CDKNIRELE TUMOR SUPPRESSOR 1) (MIS1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGSSDAGLATAAARGQVETVRQLLEAGADPNALNRFGRRPIQVMMGSAQVAELLLLHGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
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Pred. No. 1.40e-139;
11; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U66085; AAB39833.1; -.
EMBL; U66084; AAB39833.1; JOINED.
MGD; MG1:104737; CDKN2B.
THE PF00023; ANF. 3.
Cell cycle; Anti-oncogene; Repeat; ANK repeat.
                                                                                                                                                                                                                                                                                                                                                     INHIBITORS.
-1- SIMILARITY: CONTAINS 2 ANK REPEATS.
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Best Local Similarity 85.2%;
Matches 109; Conservative
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| 130 YLRTATGD 137
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                                                   CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
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MOSKaluk C.A., Hruban R.H., Liletman A., Smyrk T., Fusaro L.,
Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Rern S.E.;
Novel germline pl6iNK4 allele (Aspl45Cys) in a family with multiple
pancreatic carcinomas.";
                                                                                                                                                                                                                                                                                                         MEDILINE: 96323559.

FILZGERAID MG., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
Eltzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
Isselbacher K.J., Sober A.J., Haber D.A.;
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Familial melanoma: analysis of a clinic-based population.";
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Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148. MEDLINE; 97472457.
Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K., Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P., Fishop D.T., Bishop J.N., Germine mutations of the CDKN2 gene in UK melanoma families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glioma and carcinoma of the pancreas.";

Hum. Mutat. 12:12121212(1998).

Hum. Mutat. 12:1212-212(1998).

Hum. Mutat. 12:1212-212(1998).

Hum. Mutat. 12:1212-212(1998).

ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGILATOR OF THE PROLIFERATION OF NORMAL CELLS.

HEGTENODIMER WITH CDM4 OF CDM6.

-I- SUBBUXI: HETERODIMER WITH CDM4 OF CDM6.
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Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
Hum. Mol. Genet. 7:941-941(1998).
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Gretarsdottir S., Olafsdottir G.H., Borg A.;
Five novel somatic CDKN2/p16 mutations identified in melanoma,
                                                                                                Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,
Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach
Dracopoli N.C.;
                                                                                                                                                                                                "Mutations associated with familial melanoma impair p16INK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INHIBITORS.
-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
Mol. Genet. 4:1845-1852(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet. 6:2061-2067(1997).
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EMBL; U12820; AAB60645.1; -.
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MEDLINE; 95380169.

QUELLE D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;

"Cloning and characterization of murine pigink4a and pisink4b genes.";

"Cloning and characterization of murine pigink4a and pisink4b genes.";

Oncogene 11:635-645(1995).

-I-FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT STRONGLY DE COULD ACT AS A NEGATIVE

REGILATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.
                                                                                                                                                                                                                                                                                /FIId=VAR_001409.
A -> P (IN A LUNG TUMOR AND MELANOMA).
/FIId=VAR_001410.
A -> S (IN A BILLARY TRACT TUMOR).
/FIId=VAR_001411.
G FIId=VAR_001412.
R -> C (IN MELANOMA).
/FIId=VAR_001413.
R -> P (IN FAMILIAL MELANOMA AND MELANOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P51480;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4).
CDKN2A OR P16INK4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                  ANK MOTIF 1 (INCOMPLETE).

ANK MOTIF 2.

ANK MOTIF 3.

ANK MOTIF 3.

ANK MOTIF 4.

D -> E (IN A BILIARY TRACT TUMOR).

E -> P (IN A BILIARY TRACT TUMOR AND A FAMILIAL MELANOMA).
                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                             Repeat; ANK repeat; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FIId-VAR_001414.

E -> D (IN A BILIARY TRACT TUMOR).

FIId-VAR_001415.

L -> P (IN FAMILIAL MELANOMA).

/FIId-VAR_001416.

E -> D (IN A BILIARY TRACT TUMOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10: Indels
                                                                                                                                          4 X ANK MOTIF REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 692; DB 1; Le
Pred. No. 1.62e-126;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: remainder of annotations omitted.
                JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.8%;
larity 85.8%;
Conservative
                                                                                                           Cell cycle; Anti-oncogene;
Polymorphism; 3D-structure.
DOMAIN 12 141
EMBL; U12818; AAB60645.1;
EMBL; U12819; AAB60645.1;
EMBL; S69804; AAD14048.1;
EMBL; X94154; CAA63870.1;
PDB; 1B17; 16-FEB-99.
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                                                                                                                                                         43
75
109
141
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                                                                          MIM; 600160; -.
PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 103; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                          122
124
120
120
140
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CDN2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
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REPEAT
REPEAT
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TISSUE-THYMUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; ANK repeat; Alternative initiation.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
  SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEDPTIFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVRYLR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KIRASE 4 INHIBITOR A (CDK4I) (P16-INK4A)
(TUMOR SUPPRESSOR CDKN2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SAADRLARAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGADSN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECTION STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT STATEMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88C4588A105ECB8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.75e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBITORS.
-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                      INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 AA; 17870 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L76150; AAA85453.1; -.
MGD; MGI:104738; CDKN2A.
PFAM; PF00023; ank; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell cycle; Anti-oncogene;
DOMAIN 4 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
68
101
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15-JUL-1999
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CDN2_MONDO
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REPEAT
REPEAT
REPEAT
VARSPLIC
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셤
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                                                                                                                                                                                              EMBL: AF064808; AAC23669.1; --
EMBL: AF064808; AAC23670.1; --
EMBL: PF00023; ank; 3.

Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.

DOMAIN

4 A ANK MOTIF I (INCOMPLETE).

REPEAT 46 77 ANK MOTIF 1 (INCOMPLETE).

REPEAT 111 143 ANK MOTIF 2.

REPEAT 111 143 ANK MOTIF 3.

REPEAT 14 169 ANK MOTIF 4.

VARSPLIC 1 34 MISSING (IN SORT ISOFORM).

SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 SGEKLTEAAARGRIEVVTELLELGINPNAVNRFGRSAIQVMMMGNVRLAAILLQYGAEPN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 TPDPTILILPVHDAAREGFLDTLMLLHRAGARLDVRDSWGRLPVDLAEEQGHHLVVAYLR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okuda T., Hiral H., Valentine V.A., Shurtleff S.A., Kidd V.J., Lahti J.M., Sherr C.J., Downing J.R.;
"Molecular cloning, expression pattern, and chromosomal localization of human CDKNZD/INK4d, an inhibitor of cyclin D-dependent kinases."; Genomics 29:623-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 96362662.
Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
Zariwala M., Matera A.G., Xiong Y.;
"Isolation and characterization of pl9INK4d, a pl6-related inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homelogy to p16ink4."; Moi. Cell. Biol. 15:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 572; DB 1; Length 171;
Pred. No. 2.96e-99;
17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDN7_HUMAN STANDARD; PRT; 166 AA.
P55273; Q13102;
D1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific to CDK6 and CDK4.";
Mol. Biol. Cell 7:57-70(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.5%;
llarity 69.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 96121373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 83; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                         "Structure of the cyclin-dependent kinase inhibitor pl9Ink4d.";
Nature 389:999-1003(1997).
Nature 389:999-1003(1997).
-i - FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-i - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GARARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNVQDAS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.; "Novel INK4 proteins, pl9 and pl8, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (P18-INK4C).
CDKN2C OR CDKN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 G-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luh F.X., Archer S.J., Domaille P.J., Smith B.O., Owen D., Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
                                                                                                                                                              Chan F.K.W., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to p16ink4."; Mol. Cell. Biol. 15:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 315; DB 1; Length 166;
Pred. No. 9.05e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . -> P (IN REF. 2).
9E74F5C23B7EBCB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X ANK repeat; 3D-st
4 X ANK WOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                             Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AA; 17894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U19597; AAC52194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell cycle; Anti-oncogene;
DOMAIN 7 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.2%;
Similarity 48.2%;
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1AP7; 16-SEP-98.
MGD; MGI:105387; CDKN2D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
72
104
137
137
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STRAIN-C57BL KAPLAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                               [2]
SEQUENCE FROM N.A.
                 MEDLINE; 95257948.
                                                                                                                                                                                                                                                                                      MEDLINE; 98013176.
                                                                                                                                                                                                                                                  [3]
STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDN6_HUMAN
                                                                                                                                                                                                                                                                                                                                             Laue E.D.;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                        MEDLINE; 98455510.
Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                     Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.; "Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor pl6INK4a."; Nature 395:237-243(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQDTS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 ATPARGLVEKVRHSWEAG-ADPNGVNRFGRRAIQVMMGSARVAELLLIHGAEPNCADPA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 G-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFLAAES 130
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; ANK repeat; 3D-structure.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 2.
ANK MOTIF 4.
                                 RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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2FACD11CF56340DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDN7_MOUSE STANDARD; PRT; 166 AA. 060773; Q60773; Q60794; Q1-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 329; DB 1; I
Pred. No. 9.77e-46;
23; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                               INHIBITORS.
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U49399; AAB03772.1; -. EMBL, U40343; AAB18139.1; -. EMBL; U20498; AAAB436.1; -. EMBL; AF061327; AAC27450.1; -. PDB; 1BD8; 16-FEB-99. PDB; 1BD8; 14-OCT-98. MIM; 600927; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 46.00,
55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00023; ank; 3.
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105 1
159 1
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SEQUENCE FROM N.A.
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REPEAT REPEAT

RESULT

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REPEAT
REPEAT
SEQUENCE
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tunor suppressor INK4: determination of the solution structure of p181NK4C and demonstration of the functional significance of loops in p181NK4C and demonstration of the functional significance of loops in p181NK4C and p161NK4A.";

**Blochemistry 38:2930-2940[1999],

**INCATION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGRNUS RETINOBLASTOMA PROTEIN RB.

**INSUR SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO FOUND IN PANCREAS AND HEART.

**INSUR SAND HEART LEVELS MUSTAL MUSCLE. ALSO FOUND IN PANCREAS AND HEART.

**INTERACT.** OF THE CDKN2 WITH THE CORNATION.

**INTERACT.** OF THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE.
                                                   Matera G.A., Xiong Y.;
"Growth suppression by pl8, a pl6INK4/MTS1- and pl4INK4B/MTS2-related
"Growth subpitor, correlates with wild-type pRb function.";
Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                  Venkatazemani R., Swaminathan K., Marmorstein R.;
"Crystal structure of the CDK4/6 inhibitory protein pl81NK4c provides
insights into ankyrin-like repeat structure/function and
tumor-derived pl61NK4 mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           [5]
STROCTURE BY NWR.
MEDLINE; 99175088.
Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T., Tsai M.-D.;
                                                                                                                                                                  Blais A., Labrie Y., Poullot F., Lachance Y., Labrie C.;
Structure of the gene encoding the human cyclin-dependent kinase
inhibitor p18 and mutational analysis in breast cancer.";
Biochem. Biophys. Res. Commun. 247:146-153(1998).
          SEQUENCE FROM N.A.
MEDLINE; 95095079.
Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat; Disease mutation; 3D-structure.
                                                                                                                                                                                                                                                     MEDLINE; 96438606.
Lapointe J., Lachance Y., Labrie Y., Labrie C.;
"A p18 mutant defective in CDK6 binding in human breast cancer
                                                                                                                          SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INHIBITORS.
-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                             [4]
X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF041249; AAC39783.1; JOINED.
PDB; 11HB; 13-JAN-99.
PDB; 1BU9; PRELIMINARY.
MIM; 603369; --
                                                                                                                                                                                                                                                                                                             Cancer Res. 56:4586-4589(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF041248; AAC39782.1; -.
EMBL; AF041250; AAC39783.1; -.
EMBL; AF041249; AAC39783.1; JOI
                                                                                                                                                                                                                                         VARIANT BREAST CANCER PRO-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MINI COCCIS, ank; 3.
Cell Cycle; Repeat; ANK re
DOMAIN 5 135
REPEAT 5 36
REPEAT 69 101
REPEAT 69 101
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                                                                                                                                                   MEDLINE; 98300299.
                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98100086.
                                                                                                                                         TISSUE-BREAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOI. Cell. Biol. 15:2672-2681(1995).

-I- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGENOUS RETINOBLASTOMA PROTEIN RB.

-I- SUBUNIT: HETERROLIMER OF P18 WITH CDK6 (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                               6 GNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDL 65
                                                                                                                                                                                                                                       6 GNELASAAARGDLEQLISLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPNL 65
                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
A -> P (IN BREAST CANCER; LOSS OF CDK6
                                                                                                                                                                                                                                                                                                          66 KDRIGFA-VIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFL 122
                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPERNDENT KINASE 6 INHIBITOR (PI8-INK6) (CYCLIN-DEPENDENT KINASE 6 INHIBITOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiral H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.; "Novel INK4 proteins, p19 and p18, are specific inhibitors of cyclin D-dependent kinases CDK4 and CDK6."; Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 247; DB 1; Length 168; Pred. No. 1.11e-28;
                                                                                                                   Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Mismatches 46; Indels
                                                                                                                                                                  43; Indels
                                            /FTId-VAR_001490.
5D66AFA715186E9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC88D5489307E128 CRC64;
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ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                   Score 249; DB 1; 1
Pred. No. 4.38e-29;
28; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA
                        INTERACTION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle; Repeat; ANK repeat.

DOMAIN 5 135 4 X

REPEAT 5 36 ANK

REPEAT 37 68 ANK

REPEAT 69 101 ANK

REPEAT 102 135 ANK
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36 AN
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                                                                                                              1 25.5%;
Similarity 39.0%;
46; Conservative
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Best Local Similarity 38.20,
Compared 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:105388; CDKN2C
72
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MEDLINE; 95257948.
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                                                                                                                   Query Match
Best Local Similarity
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72
                                                                     168
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Q60772;
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ANK.
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P16157;
         MUTAGEN
SEQUENCE
                                  Query Match
DOMAIN
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBp-sib.ch).
         RDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEFLMK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.; "Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell
                                                                                                                                                                                                                                                                    Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                       SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
                                                                           JA 11
DAPK_HUMAN STANDARD; PRT; 1431 AA.
P53355;
01-0CT-1996 (Rel. 34, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
                                                                                                                                      DAPKI OR DAPK.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PRAN; PF00023; an; 8.
PFAM; PF00069; pkinase; 1.
PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 8 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X76104; CAA53712.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                               PIM: AUTOPHOSPHORYLATED
                                                                                                                                                                                                                                  Genes Dev. 9:15-30(1995).
                                                                                                                                                                                                                                                    REVISIONS TO 164-171.
                                                                                                                                                                                                                                                                                                                PROTEIN KINASES
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fransferase;
                                                 134 ATG 136
                                 125 HTA 127
                                                                                                                                                                                                                                                             Feinstein E
                                                                                                                                                                                                                                                                                                                                                                                                                              600831
                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                       DEATH.
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BINDING
ACT_SITE
DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                           517 LTASARGYHDIVECLAEHGADLNACDKDGHIALHLAVRRCQMEVIKTLLSQGCFVDYQDR 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 13:214-218(1996).

1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
BLEMENTS: BIND TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIEWHIN AND DESMIN.
ERYTHROCYTE ANYRING ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CYTOPLAGMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
                                                                                                                                                                                                                                                                                                   Lux S.E., John K.M., Bennett V.; "Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- PTM: REGULATED BY PHOSPHORYLATION.
-1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
-1- DISEASE: DEFECTS IN ANKI ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (HS).
-1- SIMILARITY: CONTAINS 24 ANK REPEATS.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96225450.

Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.,
"Ankyrin-1 mutations are a major cause of dominant and recessive
                                                                                                                                                                                                                                                                                                                                                                                       577 HGNT-PLHVACKDGNMPIVVALCEANCNLDISNKYGRTPLHLAANNGILDVVRYL 630
                                                                                                                                                                                                                                                                                                                                                                                                                               77 ATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher Chenng M.C., Ran Y.W., Palek J.;
Then sequence for human erythrocyte ankyrin.";
Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
                                                                                                                        Score 140; DB 1; Length 1431;
Pred. No. 2.39e-08;
23; Mismatches 53; Indels
                          K->A: LOSS OF ACTIVITY.
MW; 9EE84811004A155B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ANKYRIN R (ANKYRINS.2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
TISSUE-HEMATOPOLETIC;
MEDLINE; 90158830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebra
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1880 AA
DEATH DOMAIN.
                              42
160017 N
                                                                                                                               14.38;
                                                                                                                                                                                              37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 344:36-42(1990).
1397
                                                               1431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMA MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT HS ILE-462.
                                                                                                                                                             Local Similarity
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1313
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOPORM 2.2).
H -> D (IN ISOPORM 2.2).
TYCGPLEDPSELEVDIDYFMKHSKDHTSTPNP -> ELRGS GLOPDLIEGRKGAQIVKRASLKRGKQ (IN A THIRD ISOPORM).
                                                                                                                                                                                                                                                            THE BINDING OF ANKYRIN TO SPECTRIN AND THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).

24 A MAIK MOTIF (INCOMPLETE).

ANK MOTIF 1.

ANK MOTIF 5.

ANK MOTIF 6.

ANK MOTIF 10.

ANK MOTIF 10.

ANK MOTIF 11.

ANK MOTIF 11.

ANK MOTIF 12.

ANK MOTIF 13.

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ANK MOTIF 23.
                                                                                                                                PFRM; PF00023; ank; 22.
PFAM; PF00023; ank; 22.
PFAM; PF00791; 205; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Disease mutation; Elliptocytosis; Polymorphism.
                                                                                                                                                                                                              KD DOMAIN (ANION EXCHANGE PROTEIN
                                                                                                                                                                                                                                            DOMAIN).
55 KD REGULATORY DOMAIN (REGULATES
                                                                                                                                                                                                              89 KD DOMAIN (ANION EXCHANGE PI
BINDING DOMAIN).
62 KD DOMAIN (SPECTRIN BINDING
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/FTId=VAR_000601.
D -> N (IN DUESSELDORF).
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/FTId=VAR_000596.
R -> H (IN BRUEGGEN).
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E -> D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) -> E.
/FTId=VAR_000599.
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D -> E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG-VAR_000597
                                                                                                                             PS50017; DEATH_DOMAIN; 1.
                                                                  EMBL: X16609; CAA34610.1; -. EMBL: MX8800; AAA51732.1; -. PIR: S08275; SJHUK: PIR: A35049; A35049. HSSP: Q00420; IAWC. MIM: 182900; -. PROSITE; PSSO017; DEATH_DOMAIN;
                                                                                                                                                                                                                                  1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
-i- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 22 ANK REPEATS.
                                                                                                                              ..
6
                                                                                                                                                        492 NANPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRV 550
                                                                                                                                                                                                                                551 AELLLERDAHPNAAGKNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHI 607
                                                                                                                                                                                   3 EENKGMPSGGGSDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFGRRAIQVMMM-GSARV 60
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:88024; ANKI.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PRAM; PF00023; ank; 23.
PFAM; PF00531; death; 1.
PFAM; PF00791; ZUS; 1.
CYTOSKeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
DOMAIN 1 827 88 KD DOMAIN (ANION EXCHANGE PROTEIN
                                                                                                                             æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
                                                                                                  Score 140; DB 1; Length 1880;
                                                                                                            Pred. No. 2.39e-08;
25; Mismatches 55; Indels
                         729 229 A -> S (IN REF. 2).
145 1455 V -> I (IN REF. 2).
1880 AA; 206145 MW; 1C5FSE7EFDICD428 CRC64;
FTIG-VAR_000602
                                                                                                                                                                                                                                                                                                                                             ANK1_MOUSE STANDARD; PRT; 1862 AA. 202357; 01-NOY-1995 (Rel. 32, Created) 01-NOY-1995 (Rel. 39, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M84756; AAA37236.1; -. HSSP; Q00420; 1AWC.
                                                                                               y Match
Local Similarity 32.3%;
hes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
TISSUE-ERYTHROCYTE;
MEDLINE; 92345717.
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119 AEERGHRDVA 128
                                                                                                                                                                                                                                                                         608 AAKONOVEVA 617
             1698
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                                                       CONFLICT
                                          CONFLICT
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             VARIANT
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US-09-016-869A-4.rsp

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DISCLETO
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                                                                                                                                                                                                                         HAIN
       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kintner C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLUTAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- DEVELOPMENTAL STRAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.

-!- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.

-!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                              503 LHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG 562
                                                                                                                                                                                                                                                                                                                                                        Gaps
                              55 RD INJ.
55 RD INJ.
56 RD INJ.
57 RD INJ.
58 RD INJ.
58 RD ING.
58 RD INDING OF ANKTRIN TO SPECTRIN
52 X ANK MOTIF 1.
50 ANK MOTIF 1.
51 ANK MOTIF 2.
51 ANK MOTIF 4.
52 ANK MOTIF 6.
53 ANK MOTIF 6.
54 ANK MOTIF 11.
55 ANK MOTIF 11.
56 ANK MOTIF 11.
57 ANK MOTIF 12.
58 ANK MOTIF 12.
58 ANK MOTIF 13.
58 ANK MOTIF 14.
58 ANK MOTIF 15.
58 ANK MOTIF 16.
58 ANK MOTIF 16.
58 ANK MOTIF 17.
59 ANK MOTIF 16.
50 ANK MOTIF 17.
50 ANK MOTIF 18.
50 ANK MOTIF 18.
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50 ANK MOTIF 19.
50 ANK MOTIF 19.
50 ANK MOTIF 20.
50 ANK MOTIF 21.
                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                 563 KNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHIAAKQNQIEVA 614
                                                                                                                                                                                                                                                                                                                             ;
                DOMAIN (SPECTRIN BINDING
                                                                                                                                                                                                                                                                                                        Score 137; DB 1; Length 1862;
Pred. No. 7.81e-08;
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MEDLINE; 90385285.
Coffman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila notch.";
Science 249:1438-1441(1990).
BINDING DOMAIN)
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Best Local Similarity 33.9%;
Matches 39; Conservative
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PROSTIE; PRO0010; ASX_HYDROXIL; 23.
PROSTIE; PRO1010; EGF_L; 34.
PROSTIE; PS01187; EGF_C, 29.
PROSTIE; PS01187; EGF_CA; 21.
PRAM; PF00008; EGF; 36.
PFAM; PF00006; notch; 6.
Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain; Transmembrane; Signal; Glycoprotein.
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SEQUENCE OF 463-495 FROM N.A.
MEDLINE; 92009921.
TSE W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
Isolation and chromosomal localization of a novel nonerythroid ankyrin gene...;
Genomics 10:858-86(1991).
-I. FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                            Gaps
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TISSUE-BRAIN STEM;
MEDINE: 91302466.
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
AMYKRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
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Pred. No. 3.72e-07;
27; Mismatches 43; Indels
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Note: remainder of annotations omitted.
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BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHALN) TO THE CYTOPLASMIC DOMAIN OF THE REYTHROCYTES ANION EXCHANGE PROTEIN; THEY BETAIN MOST OR ALL OF THESE BINDING FONCTIONS.

ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROUGHOUT THE BRAIN.

SIMILARITY: CONTAINS 24 ANK REPEATS.
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B39643; B39643.
'; Q00420; IAWC.
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PFAM; PF00531; death; 1.
PFAM; PF00791; 2U5; 1.
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ς. Έ 464 GETALHWAARAGQVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHWAHP 523 14 SDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFGRRAIQVM-MMGSARVAELLLLHGAEP 71 Gaps 5; Score 131; DB 1; Length 1839; Pred. No. 8.05e-07; 22; Mismatches 45; Indels 524 DAATINGYI-PLHISAREGQVDVASVLLEAGAAHSLATKKGFIPLHV 569 Query Match 13.4%; Best Local Similarity 32.7%; Matches 35; Conservative 셤 ò 셤

13.4%;

Search completed: Thu Jul 20 08:39:16 2000

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:39:33 2000; MasPar time 17.39 Seconds 546.235 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-4 (1-137) from US09016869A.pep 977

1 MREENKGMPSGGGSDEGLAT.....LAEERGHRDVAGYLRTATGD 137 Sequence:

Description: Perfect Score:

225878 seqs, 69334122 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembil2
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_lnvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 42.547; Variance 77.508; scale 0.549 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | æ | | | | | |
|---------------|-------|-------|--------------------------|-----|--------|------------------------|-----------|
| Result No. | Score | Query | Query Match Length DB | DB | Q. | Description | Pred. No. |
| - | 598 | 61.2 | 98 | و ا | Q9XS52 | P15/MTS2/CDKN2B (FRAGM | 3.48e-103 |
| 8 | 586 | 90.0 | 115 | 4 | 016361 | | 1.61e-100 |
| m | 582 | 59.6 | 102 | 9 | 09x851 | P16/CDKN2A/MTS1 (FRAGM | 1.24e-99 |
| 4 | 574 | 58.8 | 168 | Ξ | P97510 | CYCLIN DEPENDENT KINAS | 7.35e-98 |
| 'n | 570 | 58.3 | 168 | Ħ | 089088 | CYCLIN DEPENDENT KINAS | 5.65e-97 |
| ø | 563 | 57.6 | 86 | Ξ | 09Z1C1 | CYCLIN-DEPENDENT KINAS | 2.00e-95 |
| 7 | 551 | 56.4 | 86 | Ħ | 054846 | CYCLIN-DEPENDENT KINAS | 8.99e-93 |
| 80 | 479 | 49.0 | 113 | Ξ | 09z1C2 | | 5.81e-77 |
| თ | 364 | 37.3 | 124 | 13 | P70067 | CDNK2X PROTEIN. | 3.36e-52 |
| 10 | 358 | 36.6 | 58 | ø | 097886 | CYCLIN-DEPENDENT KINAS | 6.26e-51 |
| 11 | 357 | 36.5 | 124 | 13 | Q9W618 | P13CDKN2X. | 1.02e-50 |
| 12 | 309 | 31.6 | | 4 | 015125 | ALTERNATIVE SPLICED FO | 1.14e-40 |
| 13 | 186 | 19.0 | 44 | Ħ | 0921C0 | CYCLIN-DEPENDENT KINAS | 3.15e-16 |
| 14 | 141 | 14.4 | 745 | 4 | 09Y544 | DJ20208.1 (NOVEL RAT E | 3.76e-08 |
| 15 | 140 | 14.3 | 1719 | 4 | 013768 | ALT. ANKYRIN (VARIANT | 5.57e-08 |
| 16 | 140 | 14.3 | 1856 | 4 | 099407 | ANKYRIN. | 5.57e-08 |
| 17 | 139 | 14.2 | 800 | S | 043988 | HOMEOBOX-CONTAINING PR | 8.24e-08 |
| 18 | 139 | 14.2 | 837 | 1 | Q63618 | ESPIN. | 8.24e-08 |
| 19 | 137 | 14.0 | 1098 | = | 961304 | ANKYRIN 1, ERYTHROID (| 1.80e-07 |
| 20 | 137 | 14.0 | 1848 | 11 | 061302 | ANKYRIN 1, ERYTHROID (| 1.80e-07 |

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musculus (Mouse).
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01-MAY-1997 (TrEMBLE) 03, Created)
01-MAY-1999 (TrEMBLE) 10, Last sequence update)
01-MAY-1999 (TrEMBLE) 10, Last sequence update)
01-NOY-1999 (TrEMBLE) 12, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4)
CPGINKAA) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
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OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGAKI K., WATARI T., TSUJIMOTO H., BASEGAWA A.;
"Cloning and chromosomal mapping of the felline genes p16(MTS1/CDKN2A)
                                                                                                                                                                                                                                                                                                                                                                                         51 QVMMMGSARVAELLILLERGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDA 110
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                                                                                               STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H., PARRY D., PETERS G., KAMB A.;
"Complex structure and regulation of the P16 (MTS1) locus.";
Cancer Res. 55:2988-2994(1995).
EMBL: S78535; AAC60650.1; -.
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P16/CDKN2A/MTS1 (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Felisa.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             Score 586; DB 4; Length 115;
Pred. No. 1.61e-100;
2; Mismatches 2; Indels
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Pred. No. 1.24e-99;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and p15(WTS2/CDKNZB).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010807; BAA33540.1; -.
                                                                                                                                                                                                                                           115 AA; 12334 MW; F5BEF54B CRC32;
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102 AA; 10824 MW; 8C3094E9 CRC32;
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Best Local Similarity 92.9%;
Matches 79; Conservative
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Best Local Similarity 95.3%;
Matches 82; Conservative
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                                                                              MEDLINE; 95330726.
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HERZOG C.R., YOU M.;
"Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
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STRAIN-DBA/2 AND C57BL/6;
MEDLINE; 95380169.
QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,
RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;
"Cloning and characterization of murine pleinK4a and plsinK4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CAST/E1, C57BL/6J AND RF/J, MOLE/EI AND MUS MUS MUSCULUS;
STRAIN-CAST/E1, C57BL/6J AND RF/J, MOLE/EI AND MUS MUS MUSCULUS;
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                             ZHANG S., RAMSAY E.S., MOCK B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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WIDDLINE; 97128825;
SOLOFE E.V., HERZOG C.R., YOU M.;
"The 5'-flanking region of the El alpha form of the murine pl6INK4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J X DBA;
MALDHBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES SERRAND M., PELLICER A., FERNANDEZ-PIQUERAS J.;
SUBmitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 574; DB 11; Length 168; Pred. No. 7.35e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DBA/2 AND C57BL/6;
GRESSANI K.M., ROLLINS L.A., MILLER M.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0444336; AAC08963.1; -
                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998)
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U66087; AAB39600.1; -.
U66086; AAB39600.1; JOINED.
AF004588; AAB61416.1; -.
                                                                                                                   STRAIN-DBA/2N; TISSUE-SPLEEN;
MEDLINE; 98151529.
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Best Local Similarity 65.0%;
Matches 80; Conservative
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U79628; AAD00226.1;
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PFAM; PF00023; ank; 3.
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SEQUENCE FROM N.A. STRAIN-SPRET/EI;
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132 RTA 134
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STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the pl6(INK4a) and pl5(INK4b) DNA sequences
in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: AF044335; AAC08962.1;
EMBL: U49279; AAC08051.1;
EMBL: U49279; AAC08051.1;
EMBL: U79626; AAD00224.1;
HSSP: PA2771; IBIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the murine Cdkn2a tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TREMBLREL. 12, Last annotation update)
01-NOV-1999 (TREMBLREL. 12, Last annotation update)
01-NOV-1999 (TREMBLREL. 12, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR PROTEIN).
PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
BURATYOCAS, Metazoas, Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Rodentla; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                  12 NCADPATLTRPVHDAAREGFLDTLVVI.HRAGARLDVRDAWGRLPVDLAEERGHRDVAGYL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 NCEDPITFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVRYL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STATUS BLANCE SPLEEN; STATUS BLANCE FROM N.A. STRAINS BLANCE STRAINS BLANCE STRAINS STRAINS S., RAMSAY E.S., MOCK B.A.; "CARARA, the cyclin-dependent kinase inhibitor encoding picinK4a and ploARF, is a candidate for the plasmacytoma susceptibility locus, Petrl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SAADRLARAAAQGRVPDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHIAALLLNYGADS 62
                                                               SAADRLARAAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGADS
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Pred. No. 5.65e-97;
22; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HERROG C.R., YOU M.; "Sequence variation and chromosomal mapping suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.2%;
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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132 RTA 134
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089088;
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SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M., PERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79637; AAD00237.1;
HSSP; P42771; 1B17.
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                                                                                                                                                                                                                                                                                                                                                                                                               Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 551; DB 11; Length 80;
Pred. No. 8.998-93;
"".mmirches 2; Indels
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Pred. No. 2.00e-95;
5; Mismatches 2; Indels
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF0154660; AAB94534.1; -.
HSSP; P42771; 1B17.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NUV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT).
0921C1 PRELIMINARY: PRT; 86 AA. 0921C1 O921C1; 0121. 0121. 0121. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0122. 0
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86 86
86 AA; 9269 MW;
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Local Similarity 91.9%;
nes 79; Conservative
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Best Local Similarity 89.5%;
Matches 77; Conservative
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64 IDKSTGATPLHDAARTGFLDTVQLLVKAGADPQARDKDNCLPIDLARQNGHTDVVAVLET 123
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Buteleostei; Acanthopterygii; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidei; Poecillidae; Xiphophorus.
                                                                                               4 EDELTTAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMGSSEVARLLLTRGADPNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 EDELTTAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMMGSSEVARLLLTRGADPNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIEDER S., CHECA-CORTES M.L., JOERG H., STRANZINGER G.;
"An equine sequence homologous to cyclin-dependent kinase inhibitor
(CDKN2A).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AGADPINGVIRFGRRAIOVMANGSARVAELLILHGAEPINCADPATUTRPVHDAARBGFL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGADPNGVNGFGRRPIQVMAMGSVHVAELLLLHGADPNRADPDTLTRPVHDAAREGFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERAIDENCE FROM N.A.
STRAIDENCE FROM N.A.
STRAIDENCE SARABEA;
STRAIDENCE S., MORIZOT D.C., DELLA COLETTA L., JOHNSTON D.A.,
WOOLCOCK B., VIEIKIND J.R., NAIRN R.S.;
"Comparative Structure and Characterization of a CDKNZ Gene in a Xiphophorus Fish Melanoma Model.";
Submitted (MAR-1999) to the EMBL/Genbank/DDBJ databases.
EMBL; AF132500; AAD21313.1;
SEQUENCE 124 AA; 13049 MW; DA386E94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalla,
Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.5%; Score 357; DB 13; Length 12
Best Local Similarity 52.5%; Pred. No. 1.02e-50;
Matches 63; Conservative 18; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 358; DB 6; Length 58; Pred. No. 6.26e-51; 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076782; AAC97110.1; ...
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NO-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                      58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE8139C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 58
58 AA; 6162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.6%;
Best Local Similarity 87.9%;
Matches 51; Conservative
      Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinase; Cyclin
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IISSUE-SKIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P13CDKN2X.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                      LT 10
097886
097886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDKN2A.
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U70634; ABD00236.1; -.
EMBL: U70634; ABT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xiphophorus maculatus (Southern platyfish).
Bukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Actinopterygil;
Neopterygil; Teleostel; Buteleostel; Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidel; Poeciliidae; Xiphophorus.
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STRXIN-JP 163 A; TISSUE-MUSCLE;
MEDLINE; 97075115.
MAIRN R.S., KAZIANIS S., MCENTIRE B.B., DELLA COLETTA L., WALTER R.B.
MORIZOT D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VMMMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 124;
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Pred. No: 5.81e-77;
13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAZIĀNĪS S., NAIRN R.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; 09273; AAB09560.3; -.
HSSP; P42771; 1BT7
SEQUENCE 124 AA; 13034 MW; BFB0B9C5 CRC32;
                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Pred. No. 3.36e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA
112 GRLPVDLAEERGHRDVAGYLRTATGD 137
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                       P16.
Mus spretus (Western wild mouse).
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112 GRLPVDLAEERGHRDVAGYLRTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GRLPLDLAQERGHQDIVRYLRSA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%;
52.5%;
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Best Local Similarity 74.7%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                        PRELIMINARY;
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Best Local Similarity
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NON_TER
SEQUENCE
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251 GHTKVLSWLLLHGGEIS-ADLWGGT-PLHDAAENGELECCQILVVNGAELDVRDRDGYTA 308
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LUX S.E., JOHN K.M., BENNETI V.;
"Analysis of CDNA for human erythrocyte ankyrin indicates a repeated
structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EENKGMPSGGGSDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFGRRAIQVMMM-GSARV 60
                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DJ202001. (NOVEL RAT ESPIN LIKE PROTEIN CONTAINING ANK REPEATS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ALT. ANKYRIN (VARIANT 2.2).
HOMO saplens (Human).
Ebkaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla; Ebtaryota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 140; DB 4; Length 1719;
Pred. No. 5.57e-08;
25; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 4; Length 745
Pred. No. 3.76e-08;
12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SECTENCE FROM N.A.
HOWDEN P.;
SUBMILTER (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031848; CAB46197.1; -.
NON_TER 745 A45
SEQUENCE 745 AA; 78960 MW; Flab0F4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00023; ank; 22.
PFAM; PF00531; death; 1.
PFAM; PF00512; 2U5; 1.
SEQUENCE 1719 AA; 189010 MW; CE3D69D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1719 AA
   745 AA
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:: || : |||
116 VDLAEERGHRDVAGYLRT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%;
Local Similarity 44.9%;
les 35; Conservative
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Local Similarity 32.3%;
les 42; Conservative
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EMBL; X16609; CAA34611.1;
HSSP; Q00421; IAWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
PRELIMINARY;
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119 AEERGHRDVA 128
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                                                                                                                                                                                   DJ20208.1 (FRAGMENT).
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Matches
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   ID ACCOUNT TO SEE THE 
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                                                                                                                                                        64 TDKSTGATPLHDAARTGFLDTVQLLVEAGADPQARDKDNCLPIDLARQNGHTDVVAVLET 123
   15 DEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSARVAELLLLHGAEPNC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINE: 97373727.
TSUBARI M., THINORN E., LAIHO M.;
TSUBARI M., THINORD E., LAIHO M.;
"Cloning and characterization of p10, an alternatively spliced in p15 cyclin-dependent kinase inhibitor.";
Cancer Res. 57:2966-2973(1997).
EMBL: AF004619; AAB69889.1; -.
HSSP; P42773; 1BU9.
SEQUENCE 78 AA; 8078 MW; 70693F9A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQV 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.6%; Score 309; DB 4; Length 78; Best Local Similarity 88.7%; Pred. No. 1.14e-40; Matches 47; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                             O15125 PRELIMINARY; PRT; 78 AA.
O15125,
O1-7AN-1998 (TTEMBLIEL. 05, Created)
O1-JAN-1998 (TTEMBLIEL. 05, Last sequence update)
O1-NOV-1999 (TTEMBLIEL. 12, Last annotation update)
ALTERNATIVE SPLICED FORM OF P15 CDK INHIBITOR.
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01-NAY-1999 (TIEMBLYel. 10, Last sequence update)
01-NOV-1999 (TIEMBLYel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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71.48;
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nes 30; Conservative
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NON_TER 44
SEQUENCE 44 AA
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